

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2003, 06:13:31 ; Search time 49.5 Seconds
(without alignments)
6418.680 Million cell updates/sec

Title: US-09-598-982-20
Perfect score: 1458
Sequence: 1 gggccccctcgagaagaat.....cgtgaagcggcgcgcgcgtcgt 771

Scoring table:
BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xjh
-O/cgpr2.1/USPTO.spool/US09598982/rnat_27012003_073716_19567/app_query.fasta_1.967
-DB=SPREMBL_21 -OPM=fastan -SUFFIX=n2p.rspc -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -UNITS=dbs START=1 -END=1 -MATRIX=blomsun62 -TRANS=human4.0.cd1
-MODE=LOCAL -OUTFMT=ptc -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USPR=US09598982 @CGN.1.1.28 @unal.27012003_073716_19567 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_oranelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviral:*
16: sp_bacterioplasmid:*
17: sp_archaeplastid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Table with 5 columns: Result No., Score, Query Match, Length, DB ID, Description. Row 1: 1, 1342, 92.0, 275, 4, Q96RZ6, Q96RZ6 homo sapien

Table with 11 columns: ID, Score, E-value, P-value, Accession, Species, Description. Row 1: Q96RZ6, 1049, 71.9, 273, Q921N4, Homo sapiens, Papilio hamadryas

ALIGNMENTS

Table with 4 columns: ID, Accession, Species, Description. Row 1: Q96RZ6, Q96RZ6, Homo sapiens, Papilio hamadryas

QY 595 GACTCCGGAGGGCCCTGTGTGCAGATGAMGGCACCTGTGCCTGACGGCGGGCGTGC
 Db 221 ASperGlygProLeuValCysLysValGluAspHrTrpLeuGlnAlaGlyVal 240

QY 655 AGCTGGGGCCGAGGGCTGTGCCAGACCACCGGGCTGGACATGCACCCCTGTCCACTAC 714
 Db 241 SerTrpGlyLugLysAlaGlnPrroAsnArgProGlyLeuTrpThrArgValThrTyr 260

QY 715 TACTTGAGCTGATGCCACACACTATGTGCCAAA 747
 Db 261 TyrLeuAspTrpTrpLeuHisArgTyrValProLys 271

RESULT 3
 Q96RZ7 PRELIMINARY: PRT: 233 AA.

ID 096RZ7
 AC 096RZ7
 DT 01-DEC-2001 (TRMBLrel. 19, Created)
 DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
 DE Mast cell tryptase beta III.
 GN TRYPTASEB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21096910; PubMed=11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 DR EMBL: AE006466; MAK61270.1; -.
 DR MEROPS: S01.027; -.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR K W HydroLase: Serine protease.
 SQ SEQUENCE 233 AA; 25874 MW; 246A96C71B2CE6D0 CRC64;

Alignment Scores:
 Pred. No.: 4.31e-70 Length: 233
 Score: 1022.00 Matches: 186
 Percent Similarity: 97.38% ConservatIve: 0
 Best Local Similarity: 97.38% Mismatches: 5
 Query Match: 70.10% Indels: 0
 DB: Gaps: 0

US-09-598-982-20 (1-771) x Q96RZ7 (1-233)

QY 19 ATGCTGGGGGTCAAGAGGGCCCGAGAGCAAGTGGCCCTGGACGTGAGAGATC 78
 Db 31 LLeValGlyGlnGlnAlaBrGArgSerLysTrpProTgHlValSerLeuArgVal 50

QY 79 CAGGGCCATAGCTGATGCACTTGTGGGGGGCTCCCATCCAGCCCGAGGGGTGTG 138
 Db 51 ArgAspArgGlyTyrTrpMenthisrheGySglYsSerLeuIlenisrProGlnrPvalLeu 70

QY 139 ACCGGCCGGGCGGTGGGGAGCCAGAGATGTGGCCCGCCCTGAGGGTGCACATG 198
 Db 71 ThrAlaAlaLanHisCysValGlyProAspRValLysAspRLeuAlaAlaLeuAdgValGlnLeu 90

QY 199 GGGAGGACAGCTGATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
 Db 91 ArgGlnGlnHisrLeuTyrGlnAspRlnLeuProValSerArgIleIleValHis 110

QY 239 CCAAGTTCATACAGCCAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 318
 Db 111 ProGlnrPheTyrThrAlaGlnIleGlyAlaAspRleAlaLeuLeuGlnGlnGlnPro 130

QY 319 GTGAGGTCTCCAGCCAGCTCCACAGGTCACCCCTGCCCTCAGAGACTTTCCC 378
 Db 131 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGlnThrPhePro 150

QY 379 CCGGGATCCCGTGGGTCACTGGCTGGGGGAGTGTGGACAAATGATGAGGGCTCCCA 438
 Db 151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGlnArgLeuPro 170

QY 439 CCGCATTTCCTGTGAAGCAGGTGAAGTCCCATTAATGAAACACATTTGTGACGCA 498
 Db 171 ProProPheProLeuLysGlnValLysValProIleMetGlnAsnHisrIleGyAspAla 190

QY 499 AAATACACACTTGGCCCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
 Db 191 LysTyrHisLeuGlnValAlaTyrThrGlyAspAspValArgIleValAlaGAspAspMetLeu 210

QY 559 TGTGCCGGAGACAGCCGGAGGAGACTCATGCCAG 591
 Db 211 CysAlaGlyAsnThrArgArgAspSerCysGln 221

RESULT 4
 Q9XSML PRELIMINARY: PRT: 273 AA.

ID Q9XSML
 AC Q9XSML
 DT 01-NOV-1999 (TRMBLrel. 12, Created)
 DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
 DE Trypsinase (EC 3.4.21.59).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RX MEDLINE=20308142; PubMed=10848900;
 RA Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D.S.,
 RA Scudamore C.L., McEwen A.R., Walls A.F., Miller H.R.P.;
 RT "cDNA sequence of two sheep mast cell tryptases and the differential
 RT expression of tryptase and sheep mast cell protease-1 in lung,
 RT dermis and gastrointestinal tract.";
 RL Clin. Exp. Allergy 30:818-883(2000).

CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.
 DR EMBL: Y18223; CAB41988.1; -.
 DR HSSP: P20231; IAAO.
 DR MEROPS: S01.118; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM00020; TRYp_SPC; 1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR K W HydroLase: Serine protease.
 FT CHAIN 29 273 TRYPTASE.
 SQ SEQUENCE 273 AA; 30156 MW; 88A19DC779053898 CRC64;

Alignment Scores:
 Pred. No.: 7.51e-70 Length: 273
 Score: 1019.00 Matches: 176
 Percent Similarity: 83.67% ConservatIve: 29
 Best Local Similarity: 71.84% Mismatches: 40
 Query Match: 69.89% Indels: 0
 DB: Gaps: 0

US-09-598-982-20 (1-771) x Q9XSML (1-273)

QY 19 ATGCTGGGGGTCAAGAGGGCCCGAGAGCAAGTGGCCCTGGACGTGAGAGATC 78
 Db 111 ProGlnrPheTyrThrAlaGlnIleGlyAlaAspRleAlaLeuLeuGlnGlnGlnPro 130

Db 29 IeIleGIyGlyGlySGLuAlaProGlySerArgTrpProTrpGlnValSerLeuArgVal 48
 QY 79 CAGGGCCATACSTGGATGACACTTCTGCGGGGGCCCTCCATCCAGCCAGATGGGTGCTG 138
 Db 49 ArgAsrGlnTrpTrpArgHisGlnCysGlySerLeuIleHisProGlnTrpValLeu 68
 QY 139 ACCGGGGGGGGTGGTGGGAGCCGGGCAAGGATCTGCGCCCGCCCTGAGGATGCACTG 198
 Db 69 ThrAlaAlaHisCysIleSerIleProIleuLeuGlnProSerAspPheArgValIlePro 88
 QY 199 CGGGAGCAGCACTTACTACCCAGCAGCAGCTGCTCCCGGTCCAGCAGGATCATCCGTGAC 258
 Db 89 ArgGlnGlnHisLeuTrpTrpGlnAspArgLeuProIleSerArgValIleProHis 108
 QY 259 CSACAGTCTACACCCGCCACATGCGGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCCG 318
 Db 109 ProHisTrpTrpMetValGlnAsnGlyIleAspIleAlaLeuLeuGlnIleuIlePro 128
 QY 319 GTGAAGGTCCTCCAGCCACACAGCGTCCACCCCTGCTCCAGAGACTTCCCC 378
 Db 129 ValSerIleSerCysHisValArgProValTrpLeuProProIleSerGlnTrpPhePro 148
 QY 379 CCGGGAGTCCCGTGGTGGTCACTGGCTGGCGGGCGATGGGACATGATGAGCGCCCTCCA 438
 Db 149 ProGlySerGlnCysTrpValTrpGlyTrpGlyAsnValAspAsnGlyArgProLeuPro 168
 QY 439 CCGCATTTCTCTGACAGCAGTGAAGTCCCATTAAGGAAACCAACCATTTGTGACGCA 498
 Db 169 ProProTrpProLeuLysGlnValLysValProIleValGlnAsnSerValCysSPTTrp 188
 QY 499 AATATACACCTTGGCGCTACACAGCGGAGCAGCGTCCCGCTCCGTCAGCAGCATGCTG 558
 Db 189 LysTrpHisSerGlyLeuSerThrAspTrpSerValProIleValGlnIleuAsnLeu 208
 QY 559 TGTGCCGGACACACCCGGAGGACTTCATGCCAGGGCAGCTCCGAGGGCCCTGGTGTGC 618
 Db 209 CysAlaGlnIleAspGlyIleTrpAspSerCysGlnGlyAspSerGlyIleProLeuValCys 228
 QY 619 AAGGTAAAGGACCTGGTGGTGGAGGGGGGGTGTGACGTGGGGGGGGGGTGTGGCCAG 678
 Db 229 LysValAsnGlnTrpTrpLeuGlnAlaGlyValValSerTrpLysAspLysAlaAsn 248
 QY 679 CCCAACCGGCTGGCATTCACACCCGCTGTCACCTTACTACTGGATGGATGCCACCACTAT 738
 Db 249 ProAspTrpProGlyValIleTrpArgIleTrpSerTrpLeuAspTrpIleHisGlnTrp 268
 QY 739 GTCCCAAAAAAGCCG 753
 Db 269 ValProGlnGlnPro 273

RESULT 5
 Q29464 PRELIMINARY: PRT: 237 AA.

AC Q29464;
 DT 01-NOV-1996 (TRMBLrel. 01, Created)
 DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
 DE Trypsase (EC 3.4.21.59) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OX
 RN (11)
 RP SEQUENCE FROM N.A.
 RC TRISUPE-LIVER CAPSULE;
 RX MEDLINE=96203914; PubMed=8620861;
 RA Pallaro M., Gambacorta A., Fiorucci L., Mignogna G., Barra D.,
 Ascoldi F.;
 RT "cDNA cloning and primary structure of trypsin from bovine mast cells
 and evidence of the expression of bovine pancreatic trypsin inhibitor
 mRNA in the same cells";
 RL Eur. J. Biochem. 237:100-105(1996).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: X94982; CAA64438.1; -
 DR HSSP: P20231; IAAO.
 DR MEROPS: S01.118; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease TRY.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS0240; TRYPIN_DOM; 1.
 DR PROSITE: PS00134; TRYPIN_HIS; UNKNOWN_1.
 DR KW Hydroxylase; Serine protease.
 FT NON_TER 1
 FT 1
 SO SEQUENCE 237 AA; 26550 MW; EA537A75294EFPBA CRC64;

Alignment Scores:
 Pred. No.: 8.62e-69 Length: 237
 Score: 1005.00 Matches: 178
 Percent Similarity: 84.32% Conserved: 21
 Best Local Similarity: 75.42% Mismatches: 37
 Query Match: 68.93% Indels: 0
 DB: Gaps: 0

US-09-598-982-20 (1-771) x Q29464 (1-237)

QY 46 AGCAAGTGGCCCTGGCAGGTGAGCCCTGAGAGTCCAGCCCATCTGATGATGACACTTCTGC 105
 Db 2 SerGlnTrpProTrpGlnValSerIleuArgValSerArgGlyTrpArgHisHisCys 21
 QY 106 GGGGGCTCCCTCATCCACCCCGATGGGTGACCGCCGGCGGTGGGAGCCGAC 165
 Db 22 GlyIleSerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProGln 41
 QY 166 GTCAAGATCTGGCCCGCCCTCAGGCTGCAACTGGGGAGGAGGAGACACTTACTACCCAGGAC 225
 Db 42 ValHisGlyProSerTrpPheArgValGlnLeuAdgGlnGlnHisLeuTrpTrpGlnAsp 61
 QY 226 CAGTGTCCCGGTGACAGCAGATCATCTGTCACCCACCAAGTCTACACCCCGCCAGATGCGGA 285
 Db 62 GlnLeuLeuProIleSerArgIleIleProHisProAsnGlyTrpSerValLysAsnGly 81
 QY 286 GCGGACATCGCCCTGAGGCTGGAGGAGACCCGGTGAAGTCTCAGCCAGCTCCACACG 345
 Db 82 AlaAspIleAlaLeuLeuGlnIleuAspLysLeuValAsnIleSerTrpHisValGlnPro 101
 QY 346 GTACCCCTGGCCCGCTCCAGAGACCTTCCCGGGGGAGTCCGGTGGGTCTACCTGAC 405
 Db 102 ValTrpLeuProGlnSerGlnTrpPheProProGlyTrpGlnCysTrpValThrIle 121
 QY 406 TGGGGGATGTGGACATGATGAGCGCCCTCCAGCCCGCCATTTCTGTGAAGCAGGTGAAG 465
 Db 122 TrpGlyAsnValAspAsnGlyArgArgLeuProProPheProLeuLysGlnValLys 141
 QY 466 GTCCCATTAATGAAAACCAATTTGTGACGGAANAATACACCTTGGGGCTTACACGGGA 525
 Db 142 ValProValValGlnAsnSerValCysAspArgLysTrpHisSerIleLeuSerTrpGly 161
 QY 526 GAGGAGTCCGGATGTCGGTCCGTCAGCAGCATGCTGTGGGGGAGCAGCCGGAGGAGCTCA 585
 Db 162 AspAsnValProIleValArgGlnAspMetLeuCysAlaGlyAspSerGlyArgAsnPhe 181
 QY 586 TGGCAGGGCAGCTCCGGAGGGCCCTGTGTGCAAGGTGAATGGCACCTGGCTGCAAGCGC 645
 Db 182 CysGlnGlyAspSerGlyIleProLeuValCysLysValAsnGlyThrTrpLeuGlnAla 201
 QY 646 GGGGTGGTAACTGGGGCGAGGGCTGTGCCAGACCCCAACCGGCTTGGCATTCACACCCGT 705
 Db 202 GlyValValSerTrpGlyAspGlyCysAlaLysProAsnArgProIleTrpTrpArg 221
 QY 706 GTACACTTACTTGGATGAGTCCACACCACTATGTCACCCCAAAAAAGCCG 753
 Db 222 ValThrSerTrpLeuAspTrpIleHisGlnTrpValProGlnGlnPro 237

QY 259 CCACAGTTCTACACSSCCAGATCCGAGCGGACATCCSCCTGAGCTGGAGGAGCCG 318
 Db 111 ProGlnPrHeuYlLeIleGlnPrGlyAlaAspRIleAlaLeuLeuGluLeuGluPuRo 130
 QY 319 GTGAAGSTCCAGCCAGCCAGTCCACAGCTCCSCCTGAGCTGGAGGAGCCG 378
 Db 131 ValAsnIleSerSerHisIleHisThrValIThrLeuProGlnIleSerGluThrProGly 150
 QY 379 CGGGGATGCGCTGGGTCAGTCCGTCGGGCGATGTCGAGCAATGAT 426
 Db 151 ProGlyMeuProCysTrpValIThrGlyAspValAspAsn 166

RESULT 8
 Q8TD16 PRELIMINARY: PRT: 130 AA.

AC 08TD16: 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Delta I tryptase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hunt J.E., Mang H.W., Thomas P.S., McNeil H.P.:
 RT "Cloning and characterization of novel human tryptase cDNAs."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF421357; AAL86695.1; -
 FT NON_TER 1 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA: 14765 MW; E2E59C4344AF3260F CRC64;

Alignment Scores:
 Pred. No.: 8.18e-42 Length: 130
 Score: 651.50 Matches: 117
 Percent Similarity: 87.05% ConservatIve: 4
 Best Local Similarity: 84.17% Mismatches: 9
 Query Match: 44.68% Indels: 9
 DB: Gaps: 1

US-09-598-982-20 (1-771) x Q8TD16 (1-130)
 QY 25 GGGGGTCAGGAGGCGCCCGAGCAAGTCCGTCGAGCTGGAGGAGCCG 84
 Db 1 GtYgIyGlnGlnAlaIleProGlySerIyStrPrGlnValSerLeuArgIyAla 20
 QY 85 CCATACSTGATGACSTTTCGCGGGGCTCCATCCACCCSCAGTGGCTGAGCCG 144
 Db 21 ProYtYTrMeuHisrheCysGlySerLeuIleHisProGlnIThrValLeuThrAla 40
 QY 145 GCGGCGTCCGTCGGGACCGAGCTCAAGATCTGGCCGCTGAGGCTGACTGGCGGAG 204
 Db 41 AlanHisCysMeuSerIyPro-----ValGlnIleuArgIy 51
 QY 205 SAGKACSTTACTACAGGAGGAGGAGGTCGCGGTCAGAGGATCATGTCGAGCCAG 264
 Db 52 GlnHisLeuYlLeuYlLeuIleHisProGlnValSerIleIleValHisProGln 71
 QY 265 TTTCACCCGCGCCAGATCCGAGGAGGAGGTCGCGGTCAGAGGATCATGTCGAGCCAG 324
 Db 72 rHeuYlLeIleGlnIThrGlyAlaAspRIleAlaLeuLeuGluLeuGluPuRoValAsn 91
 QY 325 GTTCGAGCCAGCCAGCCAGGCTCCAGCTCCSCCTGAGCTGGAGGAGCCG 384
 Db 92 IleSerSerHisIleHisThrValIThrLeuProGlnIleSerGluThrProGly 111
 QY 385 AAGCCGCTGGTGGTACSTCCGTCGGGCGATGTCGAGCAATGATGAGGCTCCAGCCAG 441
 Db 112 MetProCysTrpValIThrGlyAspValAspAsnValHisLeuProPro 130

RESULT 9
 Q8SQ44 PRELIMINARY: PRT: 277 AA.

AC 08SQ44: 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DR 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Tryptase precursor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Sato M., Yoshida S., Iida K., Tomozawa T., Kido H., Yamashita M.:
 RT "A Novel Influenza A Virus Activating Enzyme from Porcine Lungs:
 RT Purification and Characterization."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB080655; BAB85761.1; -
 KW Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 277 TRYPTASE.
 SQ SEQUENCE 277 AA: 30407 MW; 35FC8B569C0EDB4C5 CRC64;

Alignment Scores:
 Pred. No.: 1.02e-41 Length: 277
 Score: 651.00 Matches: 126
 Percent Similarity: 66.27% ConservatIve: 39
 Best Local Similarity: 50.60% Mismatches: 76
 Query Match: 44.65% Indels: 8
 DB: Gaps: 3

US-09-598-982-20 (1-771) x Q8SQ44 (1-277)
 QY 19 ATCTGGGGGTCAGGAGGCGCCCGAGCAAGTCCGTCGAGCTGGAGGAGCCG----- 72
 Db 31 ILeValGlnGlnHisAspValSerIyTrpYlProTrGlnValSerLeuArgIySer 50
 QY 73 ---AGAGTCAGGCGCCAGATCCGATCCGCTCCGCGGGGCTCCATCCAGCCCGCG 129
 Db 51 YrYrGValIyLeuGlnYlArgYrPrMeuHisrheCysGlySerLeuValHisProGln 70
 QY 130 TCGGTCSTGACCGCCCGGCTCCGTCGAGGAGCCGAGCTCAAGATCTGGCCGCTGAG 189
 Db 71 TrpValIleuThrAlaIleHisCysValAspSerHisAsnLeuYlProGlnAspValArg 90
 QY 190 GTGCACATCCGCGGAGGAGGAGCTTACTACTACAGCAAGTCCGTCGAGCTGGAGGAGCCG 249
 Db 91 ValGlnValGlnIleuYlSerIyTrpYlArgYrPrGlnIleuThrIyValIyGlnIle 110
 QY 250 ATCTGGACCCAGATCTTAC---ACCGCCAGATCCGTCGAGGAGCCGCTGAGGAG 306
 Db 111 IleArgHisProIyStrIyIleuYlRheAlaIyGlnGlnIleAlaLeuIleuGln 130
 QY 307 CTGCAGAGCCGCGTAAAGCTTCCAGCCAGCTCCAGGAGCTCCAGCTCCGCTGAGCA 366
 Db 131 LeuGlnAlaProIleuThrIleuSerAlaArgValAsnValIyGlnIleValIleValHis 150
 QY 367 GAGACSTTCCCGCGGAGATCCGTCGAGGAGCTCCAGCTCCGCTGAGGAGGAGCAATGAT 426
 Db 151 LeuYlValIProIyGlnYlYlSerIyCysSerValIThrGlnYlYlAsnIleYlHisAsn 170
 QY 427 GAGCGGCTCCAGCCAGATCCGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486
 Db 171 LeuSerLeuProIyProIyTrHisLeuGlnGlnValIleValIleValIleValHis 190
 QY 487 ATTTGTGACGCAAAATACACCTTGGCGCTCCAGCGGAGGAGGAGGAGGAGGAGGAGGAG 546
 Db 191 ValCysAsnIyHisIyTrGly-----ThrGlnYlProAsnSerIyProIleYl 206
 QY 547 GACGACATGCTTGTCCGCGGAGCAACCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 606

Db 207 ALaarpmLleuCySaLaGlySerLysGlyLeuAspSerCysGlnGlyAspSerGlyGly 226
 Qy 607 CCCCTGCTGTCGAAGATGAAATGCAACCTGGCTGCAAGCGCGCTGGTACGTGGGCGAG 666
 Db 227 ProLleuMeCysSerTrpAsnGlyThrTrpValGlnValGlyIleValSerTrpGlyArg 246
 Qy 667 GGCCTGTCGCCAAGCCCAACCGCGCTGGCATCTACACCCGTCGACCACTTGGACTGG 726
 Db 247 GTCySGlyLeuNH1AsnPherProGlyValTyrIleArgValMetSerTyrValSerTrp 266
 Qy 727 ATCCACCACTATGTCGCCCAAAAAGCCG 753
 Db 267 IleTyrGlnTyrValProArgSerPro 275
 RESULT 10
 Q99MS4 PRELIMINARY: PRT: 279 AA.
 AC 099MS4
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Implantation serine proteinase 2.
 GN ISP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21361749; PubMed=11467974;
 RA "O'Sullivan C.M., Liu S.Y., Rancourt S.L., Rancourt D.E.;
 RA "Regulation of the trypsin-related proteinase ISP2 by progesterone in
 RA endometrial gland epithelium during implantation in mice.";
 RL Reproduction 122:235-244 (2001).
 RN [2]
 RE SEQUENCE FROM N.A.
 RC STRAIN=BAUB/C; TISSUB=UTERUS;
 RA Shen Q.-X., Wang J., Huang Z.-P.;
 RA "Identification of endometrial factors involved in mouse embryo
 RA implantation.";
 RL Submitted (NOV-2001) to the EMBL/Genbank/DDIJ databases.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.
 DR EMBL: AF305425; AAK15264.2; -
 DR EMBL: AF442819; AAL38005.1; -
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.315; -
 DR MGD: MGI:2149952; ISP2.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_SIS; UNKNOMN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Serine protease.
 SQ SEQUENCE 279 AA; 30986 MW; 81C43A59935244D7 CRC64;

Db 51 TyrArgTyrTyrTrpAlaPheTrpValHisAsnCySgIyGlySerIleIleHisProGln 70
 Qy 130 TGGGTTCATACCCGCGCGCGCTGCGGGAGCCGACCGTCAAGATTCGCCCCCTCAGG 189
 Db 71 TrpValLeuThrValAlaHisCysIleArgGluArgAspAlaSerProSerValPheArg 90
 Qy 190 GTCACATCCGCGAGCAGCAGCCTTACTACAGACCCACAGCAGCAGCAGCAGCAGCAGC 249
 Db 91 IleArgValGlyGluAlaIleTyrLeuTyrGlyGlyGlnLeuLeuSerValSerArgVal 110
 Qy 250 ATCGTCACCCCAACAGTTCATACACCCGCGAGATCCGAGCCGACATCCGCTGGAGCTG 309
 Db 111 IleIleHisProAspPheValHisAlaGlyLeuGlySerAspValAlaLeuGlnLeu 130
 Qy 310 GAGAGCCGCGTGAAGTCTCCAGCCACGTCACAGCAGCAGCAGCAGCAGCAGCAGC 369
 Db 131 AlaValSerValGlnSerPheProAsnValLysProValLysLeuProSerGlnSerLeu 150
 Qy 370 ACCCTTCCCGCGCGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 Db 151 GluValThrLysLysAspValCysTrpValThrGlyTyrPheValAlaValSerThrHisArg 170
 Qy 430 CGCCTCCACCCGCGCATTCCTCTGAAGCAGGTCGAAAGTCCCAATATGAAAAACACATT 489
 Db 171 SerLeuProProTyrArgLeuGlnGlnValGlnValLysIleIleAsnSerLeu 190
 Qy 490 TGTGAGCCAAATATCCACCTGGCGCC---TACAGCGGAGAGCAGCAGCAGCAGCAGC 546
 Db 191 CysGlnGlnMetTyrHisAsnAlaThrArgHisArgAsnArgGlyGlnIleHisIleLeu 210
 Qy 547 GACGACATCTGCTGCTGCGGGAACACCCGAGGACTCATCCAGCGGCGGCGGCGGCGG 606
 Db 211 LysAspMetLeuCySaLaGlyAsnGlnGlyGlnAspSerCysTyrGlyLysSerGlyGly 230
 Qy 607 CCCCTGCTGTCGAAGTGAATGGCACCTGCTGCACAGCGCGCGCTGGTCACTGGGCGAG 666
 Db 231 ProLeuValCysAsnValThrGlySerTrpThrLeuValGlyValAlaValSerTrpGlyTyr 250
 Qy 667 GGCCTGTCGCCAAGCCCAACCGCGCTGGCATCTACACCCGTCGACCACTTGGACTGG 726
 Db 251 GTCySaLaLeuArgAspPheProGlyValTyrAlaArgValGlnSerPheLeuProTrp 270
 Qy 727 ATC 729
 Db 271 Ile 271
 RESULT 11
 Q96RZ8 PRELIMINARY: PRT: 321 AA.
 AC 096RZ8
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE HS transmembrane tryptase, gene name TMR, AF175522_1.
 GN TRPA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21096910; PubMed=11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RA "Sequence, structure and pathology of the fully annotated terminal 2
 RA Mb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 DR EMBL: AE006466; AAK61269.1; -
 DR MEROPS: S01.028; -
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.

DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 KW Hydrolase: Serine protease; Transmembrane.
 SQ SEQUENCE 321 AA; 33829 MW; PFF50899EDCA4C73D CRC64;

Alignment Scores:
 Prod. No.: 5.23e-37 Length: 321
 Score: 589.50 Matches: 118
 Percent Similarity: 61.89% Conservative: 33
 Best Local Similarity: 48.36% Mismatches: 80
 Query Match: 40.43% Indels: 13
 DB: Gaps: 6

US-09-598-982-20 (1-771) x Q96RZ8 (1-321)

OY	16	AGAAATCGGCGGGGAGGAGGCCCCAGGAGGAAAGTGGCCCTGGAGGAGCTGAGCA	75
DB	37	Arg1Leu1Gly1Gln1His1Ala1Pro1Ala1Gly1Ala1Trp1Pro1Trp1Gln1Ala1Ser1Leu1Arg	56
OY	76	GTCCACGGCCCATAGTACTGGATGCATCTTCTGCGGGGGCTCCCTATCCACCCCGAGTGGGTG	135
DB	57	Leu1Arg1Arg1-----Val1His1Val1Gly1Gly1Ser1Leu1Leu1Ser1Pro1Gln1Trp1Val	73
OY	136	CTGACCGCGCGCGGGGTGGTGGGAGCCGAGCTCAAGATCTGGCCCGCTCAAGGGTGC	195
DB	74	Leu1Thr1Ala1Ala1His1Cys1Rhe1Ser1Gly1Ser1Leu1Asn1Ser1-----Ser1Asp1Trp1Gln1Val1His	92
OY	196	CTGGCGGGGAGGAGCCACTACTACAGGAGCCAGTCTGCGCGGTCCAGGAGGATCAATCTGTG	255
DB	93	Leu1Gly1Gln1Leu1Gln1Ile1Thr1Leu1Ser1Pro1His1Rhe1Ser1Thr1Val1Arg1Gln1Ile1Leu	112
OY	256	CACCCACAGTTCTACACCCGCCAGATCCGGA-----GGCAGATCGCCCTGCTGGAGCTG	309
DB	113	His1Ser1Ser1-----Pro1Ser1Gly1In1Pro1Gly1Thr1Ser1Gly1Ala1Leu1Val1Gln1Leu	131
OY	310	GAGAGCCGGGTGAAGSTCTCCAGCCAGCTCCACAGGTTACCCCTGCCCTCCAGAG	369
DB	132	Ser1Val1Pro1Val1Thr1Leu1Ser1Ser1Arg1Ile1Leu1Pro1Val1Cys1Leu1Pro1Gln1Asn1Ser1Asp	151
OY	370	ACCTTCCCGCCGGGGAGTCCGTGGGTTCACTGGCTGGCGGATGTGGCAATGATGAG	429
DB	152	Asp1Rhe1Cys1Pro1Gly1Ile1Arg1Cys1Trp1Val1Thr1Gly1Trp1Gly1Trp1Arg1Gln1Gly1Gln	171
OY	430	CGCCTCCACCCGATCTCTGTGAAGCAGTGAAGTCCCAATGAAATGGAAACACACAT	489
DB	172	Pro1Leu1Pro1Pro1Pro1Tyr1Ser1Leu1Arg1Gln1Val1Val1Ser1Val1Val1Asp1Thr1Gln1Thr	191
OY	490	PTGACGAAATAATACCACTTGGCCCTTACAGGGAGAGAGAGCTCCCGCATPGCCGCTGAC	549
DB	192	Cys1Arg1Arg1Asp1-----Tyr1Pro1Gly1Pro1Gly1Ser1Ile1Leu1Gln1Pro	206
OY	550	GACATGCTGTGTCGGCGGAAACACCCGGAAGGACTATGCCAGGAGGACTCCGAGGGGCC	609
DB	207	Asp1Met1Leu1Cys1Ala1Arg1Gly1Pro1---Gly1Asp1Ala1Cys1Gln1Asp1Ser1Arg1Gly1Pro	225
OY	610	CTGGTGTGCAAGGTGAATGGACCTGGCTGCAGAGCCGGCGTGGTCAAGTGGGGCCAGGC	669
DB	226	Leu1Val1Cys1Gln1Val1Asn1Gly1Ala1Trp1Val1Gln1Ala1Gly1Ile1Val1Ser1Trp1Gly1Gln1Gly	245
OY	670	PTGCGCCACCCCAACCCGGCTGGCATCTACCCCTGTGACCCCTACTACTTGGACPTGGATC	729
DB	246	Cys1Gly1Arg1Pro1Asn1Arg1Pro1Gly1Val1Trp1Thr1Arg1Val1Pro1Ala1Trp1Val1Asn1Trp1Ile	265
OY	730	CACCACTATGTC 741	
DB	266	Arg1Arg1His1Ile 269	

RESULT 12
 Q924N9 PRELIMINARY: PRT: 274 AA.
 AC Q924N9: 01-DEC-2001 (TRYPsin.Dom, 19, Created)
 DT 01-DEC-2001 (TRYPsin.Dom, 19, Last sequence update)

DR 01-JUN-2002 (TRYPsin.Dom, 21, Last annotation update)
 DE Implantation serine proteinase.
 GN ISPL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD1
 RX MEDLINE=21319572; PubMed=11425330;
 RA O'Sullivan C.M.; Rancourt S.L.; Liu S.Y.; Rancourt D.E.;
 RT "A novel murine trypsinase involved in blastocyst hatching and
 outgrowth";
 RL Reproduction 122:61-71(2001).
 DR EMBL; AF184895; AAK84171.1; .
 DR MEROPS; S01.314; .
 DR MGD; MGI:2149951; Ispl.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; Trypsin_1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; UNKNOWN_1.
 KW Hydrolase: Serine protease.
 SQ SEQUENCE 274 AA; 30628 MW; 47CCD1E2C4ABBB55 CRC64;

Alignment Scores:
 Prod. No.: 2.24e-35 Length: 274
 Score: 568.00 Matches: 110
 Percent Similarity: 60.25% Conservative: 37
 Best Local Similarity: 45.08% Mismatches: 93
 Query Match: 38.96% Indels: 4
 DB: Gaps: 2

US-09-598-982-20 (1-771) x Q924N9 (1-274)

OY	19	ATCGTCCGGGGGTGAGGAGGCCCCAGGAGGAAAGTGGCCCTGGAGGAGCTGAGAGTC	78
DB	31	Ile1Val1Gly1Gln1Arg1Thr1Pro1Gly1Lys1Trp1Pro1Trp1Gln1Val1Ser1Leu1Arg1Met	50
OY	79	CACGGC-----CAATAGTGCATCTTCTGCGGGGGCTCCCTCAATCCACCCGAG	129
DB	51	Tyr1Ser1Trp1Gln1Val1Asn1Ser1Trp1Val1His1Ile1Cys1Gly1Ser1Ile1His1Pro1Gln	70
OY	130	TGGGTGTGACCCCGCCGGCTGGGAGCCGAGCTGAAGATGTCGCGCCCTCAGG	189
DB	71	Tyr1Ile1Leu1Thr1Ala1His1Cys1Ile1Gln1Ser1Gln1Asp1Ala1Asp1Pro1Ala1Val1Arg1Arg	90
OY	190	GTGCAACTGGCGGAGGAGGAGCCCTACTACGAGGAGCAAGCTCTGCGCGGTCCAGAGATC	249
DB	91	Val1Gln1Val1Gly1Gln1Val1Trp1Leu1Trp1Lys1Gln1Gln1Leu1Leu1Asn1Ile1Ser1Arg1Ile	110
OY	250	ATCGTCCACCCGATCTCTGTGAAGCAGTGAAGTCCCAATGAAATGGAAACACACAT	309
DB	111	Ile1Leu1His1Pro1Asp1Trp1Asn1Asp1Val1Ser1Lys1Arg1Rhe1Leu1Ala1Leu1Met1Gln1Leu	130
OY	310	GAGGAGCCGGTGAAGSTCTCCAGCCAGCTCCACAGGTTACCCCTGCCCTCCAGAG	369
DB	131	Thr1Ala1Leu1Leu1Val1Thr1Ser1Thr1His1Val1Ser1Pro1Val1Ser1Leu1Pro1Lys1Asp1Ser1Ser	150
OY	370	ACCTTCCCGCCGGGAGTGGCCGTTGCTGGTCACTGGCTGGCGGATGGGACAAATGATGAG	429
DB	151	Thr1Rhe1Asp1Ser1Thr1Asp1Gln1Cys1Trp1Leu1Val1Gly1Trp1Gly1Asn1Leu1Gln1Arg1Val	170
OY	430	CGCCTCCACCCGATCTCTGTGAAGCAGTGAAGTCCCAATGAAATGGAAACACACAT	489
DB	171	Pro1Leu1Gln1Pro1Trp1Gly1Gln1His1Gln1Val1Lys1Ile1Pro1Ile1Gln1Asp1Lys1Ser	190
OY	490	PTGACGAAATAATACCACTTGGCCCTTACAGGGAGAGAGAGCTCCCGCATPGCCGCTGAC	549
DB	191	Cys1Lys1Arg1Ala1Arg1Arg1Lys1Ser1Ser1Arg1Lys1Ile1Val1Ala1Ala1Ile1Rhe1Asp	210
OY	550	GACATGCTGTGTCGGCGGAAACACCCGGAAGGACTATGCCAGGAGGACTCCGAGGGGCC	609

Db 211 AspmellucysalaglYhrserglYaraglYproCyspneGlyASPserCdiGlylPro 230
 OY 610 TGTCGTGGAGGATGATGGACCTGGCTGGAGCGGGCGGCTGTACGGGGGCGAGGGC 669
 Db 231 LeuValGyTrrPlySserAsnlySrrPllleGlnValGlyValSerlySGlylLeasp 250
 OY 670 TGTGGCCAGCCCAACCGCGCTGGCATTCACACCCCGTGTACCTACTACTGAGCTGATC 729
 Db 251 CysSerAsn---AsnLeuProserIlePheSerArgValGlnSerSerLeuAlaIrrPile 269
 OY 730 CACCACATATGC 741
 Db 270 HisGlnHisIle 273

RESULT 13
 O96L36 PRELIMINARY; PRT; 115 AA.
 AC O96L36;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Delta I tryptase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hunt J.E., Wang H.W., Thomas P.S., McNeill P.;
 RT "Cloning and characterization of novel human trypsinase cDNAs."
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY055427; AAL17874.1;
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PROSITE: PS0240; TRYPSIN_DOM. 1.
 DR DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolyase; Serine protease.
 FT NON_TER 1 1
 FT NON_TER 115 115
 SO SEQUENCE 115 AA; 12994 MW; E56C3C592D01BBE9 CRC64;

Alignment Scores:
 Pred. No.: 3.23e-34 Length: 115
 Score: 552.00 Matches: 100
 Percent Similarity: 92.17% Conservatve: 6
 Best Local Similarity: 86.96% Mismatches: 9
 Query Match: 37.86% Indels: 0
 Gaps: 0

US-09-598-982-20 (1-771) x O96L36 (1-115)

OY 112 TCCCTCATGCCACCCCGATGGGTGTGACCCCGCGCGTGGTGGACCGAGCTGAAG 171
 Db 1 SerLeuIleHisPrgIlnTrValleuThrAlaAlaHisCysmetGlnPrrAspIleLys 20
 OY 172 GATGTGGCCCGCTCAGGCTGCACTGGCGGAGAGCGACCCCTACTACTACAGGAGCGTGG 231
 Db 21 AspLeuAlaAlaLeuAlaArgValGlnLeuArgGlnGlnHisLeuTyrTTrGlnAspIlnLeu 40
 OY 232 CTGGCGGTACAGGAGGATCGTGCACCCACAGTTCACACCCCGCCAGATCCGAGCGAGC 291
 Db 41 LeuProValSerArgIleIleValHisPrgIlnPheTyrIleIleGlnThrGlyAlaAsp 60
 OY 292 ATCGCCCTGTGGAGCTGGAGGAGCGCGGTGAAGGTCTCCAGCCAGCTCCACACCGTGGC 351
 Db 61 IleAlaLeuLeuGlnLeuGlnLeuGlnProValAsnIleSerSerHisIleHisThrValThr 80
 OY 352 CTGGCCCGCTCAGAGAGCTTCGCCCGGGGATGGCGTGGTGGTGCATGGCGGGG 411
 Db 81 LeuProProAlaSerGluThrPheProProGlyMetProCysTrrValThrGlyTrrPgly 100
 OY 412 GATGTGACAAATGATAGAGCGCTCCACCCGCAATTTCTCTGAAG 456

Db 101 AspValAspAsnValHisLeuProSerProTrrProLeuLys 115
 RESULT 14
 O8R1A6 PRELIMINARY; PRT; 331 AA.
 AC O8R1A6;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RIKEN cDNA 2010001P08 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC024903; AAH24903.1;
 SO SEQUENCE 331 AA; 35639 MW; C06F6F2FA261636 CRC64;

Alignment Scores:
 Pred. No.: 1.58e-33 Length: 331
 Score: 544.00 Matches: 109
 Percent Similarity: 59.30% Conservatve: 44
 Best Local Similarity: 42.25% Mismatches: 91
 Query Match: 37.31% Indels: 14
 Gaps: 7

US-09-598-982-20 (1-771) x O8R1A6 (1-331)

OY 16 AGAATCGTGGGGGTGACAGAGGCGCCCAAGAGAGAGTGGCCCTGGAGCTGAGCTGAGA 75
 Db 53 ArgIleValSerGlyGlnAspAlaGlnLeuGlyA9GtrPrrPrrGlnValSerValArg 72
 OY 76 CTCACAGCCGCTACTGTGATGCATTCGCGGGGGCTCCCGTACCCCGCCAGTGGGTG 135
 Db 73 GlnAsnGly-----AlaHisValCysGlyGlySerLeuIleAlaGlnAspPrrVal 89
 OY 136 CTGACCGCGCGCGCGTGGTGGAGCGGACGTCAAGAGTCTGGCCCGCTCAGGCTGCA 195
 Db 90 LeuThrAlaAlaHisCysPheAsnGlnGly---GlnSerLeuSerIleTyrThrValLeu 108
 OY 196 CTGGCGGAGACACCTACTACTACAGAGC-----CAGCTGTGGCGGTGAGC 243
 Db 109 LeuGlyThrIleSerSerTyrPrgIlnAspAsnGlnPrrGlyGlnLeuAlaValAla 128
 OY 244 AGGATCATGCTGCACCCACAGTTCACACCGCC-----CAGATCGGAGCGGACATCGCC 297
 Db 129 GlnPheIleLysHisPrrSer---TyrSerAlaAspGlnHisSerSerGlyAspIleAla 147
 OY 298 CTGTGTGAGCTGGAGAGCGCGGTGAAGTCTCCACAGCTCCACAGGCTGACCCCTGGCC 357
 Db 148 LeuValGlnLeuAlaSerPrrIleSerPheAsnAspTyrIleLeuPrrValAlaCysLeuPrr 167
 OY 358 CTTGGCTGAGAACCTTCCCGCGGGGAGTGGCGTGGTGGTGGTGGTGGGCGGATGG 417
 Db 168 LysPrrGlyAspPrrLeuAspPrrGlyThrMetCysTrrValThrGlyTrrPrrIleHisIle 187
 OY 418 GACAATGATAGCCGCTCCACCGCCGATTCCTCTGAAGAGCAGGTAAGTCCCAATATG 477
 Db 188 GlnThrAsnGlnPrrLeuPrrPrrPrrPrrPrrLeuGlnGlnValPrrLeuIle 207
 OY 478 GAANAACCAATTTGTGACGCAAAATACCACTTGGCGCTACACGAGAGACAGCTGGCC 537
 Db 208 AspAlaGlnThrCysAsnAsnThrTyrTrrGlnGlnAsnSerIlePrrGlyThrGln---Pro 226
 OY 538 ATGTCGCGTGGAGACATGCTGTGGCCGGG-----AACACCGCGGAGGAGCTCAAGCCAG 591
 Db 227 ValIleLeuGlnGlyMetLeuCysAlaGlyPheGlnGlnGlyLysLysAspAlaCysAsn 246

```

QY 592 GCGACCTCGGAGGGCCCGCTGTGTGCAAGTGAATGGCACCTGGCTGCAGCGGGCGGTG 651
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 G1YAspSerG1Yg1YPrOleuValCYsAspIleAsnAspValTTrPleGlnIaG1YVal 266

QY 652 GTACAGTGGGGGAGGGGCTGTGTGCCCAACCGGCTGGCATCTACACCGCTGTGCACC 711
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 ValSerTrpG1YSerAspYsAlaLeuPheLYsArGProG1YValTyrThrAsnValSer 286

QY 712 FACTACTGTGGATGCACCATATGTGCCCAAAAAGCGGTGAAGCGCGCCG 765
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 ValTyrIleSerTTrPleGlnAsnThrMetTTrPAsnLeuProMetG1UG1YArg 304

RESULT 15
Q9PVX7 PRELIMINARY: PRT: 389 AA.
AC Q9PVX7
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DR 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
DE Epidermis specific serine protease.
GN XEPSIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83395;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K.:
RT "The expression control of xepsin by non-axial and planar
  RT post-erolizing signals in Xenopus epidermis."
RL Submitted (0CT-1998) to the EMBL/GenBank/DDJB databases.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
  CC TRYPsin FAMILY.
DR EMBL; AB018694; BAA84941.1; -
DR HSSP; P00763; LDPO.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease TRY.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW HydroLase; Protease; Serine protease.
SQ SEQUENCE 389 AA; 42375 MW; B31FBA42F5D1F6E3 CRC64;

```

US-09-598-982-20 (1-771) x Q9PVX7 (1-389)

Alignment Scores:

```

Pred. No.: 1.94e-33 Length: 389
Score: 543.00 Matches: 108
Percent Similarity: 57.14% Conservative: 36
Best Local Similarity: 42.86% Mismatches: 96
Query Match: 37.24% Indels: 12
DB: 13 Gaps: 5

```

```

QY 7 CTGCGAAGAAATGCTGGGGGCTCAGAGAGCCCGCCAGAGCAAGTGGCCCTGCAGAGTG 66
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22 IleSerAsnArG1IleValG1Yg1YMetAspSerLYsArG1Yg1YTrProTrrPrlnIle 41

QY 67 AGCCTGAGAGTCCAGCGCCCATATCGATGACATTCCTGGGGGCTCCCTCATCCACCC 126
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 SerLeuSerTyrLYsSerAsp-----SerIleCYsG1Yg1YSerLeuLeuThrAsp 58

QY 127 CAGTGGGTCTGACCGCCCGCGGTGCGTGGAGCGGACGTCGAAGATCTGGCCCGCTC 186
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 SerTTrpValMetThrAlaIaHisCYsIle-----AspSerLeuAspValSerTyrTyr 76

QY 187 AGGTGCAACTCGCGGAGCAGCAGCCTTACTACTCAGAGCAGCAAGCTGCTGCGGTCA 246
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 ThrValTyrLeuG1YAlaTyrG1nLeuSerAlaProAspAsn--SerThrValSerTyr 95

```

```

QY 247 -----ATCATCGTGCACCCCAAGTCTTCAACCGCCCAAGATCGAGCGGACATC 294
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 G1YValLYsSerIleThrLYsHisProAspPheG1nTyrG1UG1YSerSerG1YAspIle 115

QY 295 GCCCTGTGGAAGCTGTGAGAGAGCCCGTGAAGGTCTTCCACAGCCAGCTCCACACCGT 354
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 AlaLeuIleG1nLeuG1nLYsProValThrPheThrProTyrIleLeuProIleCYsLeu 135

QY 355 CCCCGCTCAGAACCTTCCCGCCCGGGGATCGCGGTGGTGTACMGCGTGGGGGAT 414
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 ProSerG1nAspValG1nPhenAlaIaG1YThrMetCYsTTrpValThrG1YTrP1YsN 155

QY 415 GTGCAAAATGATGAGCGCCCTCCACCGCCATTTCCCTGTAAGCAGGTGAAGTCCCAT 474
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 IleG1nG1UG1YThrProleuIleSerProLYsTTrIleG1nLYsAlaG1YValAlaIle 175

QY 475 ATGAAACACATTTGTGAGCGCAAAATPACACCTTGGCGCTACACGGAGACGAGCTC 534
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 IleAspSerSerValCYsG1YThrMetTyrG1nSerSerLeuG1YTrIleProAspPhe 195

QY 535 CGCATCGTCCCGACGACATGCTGTGCGCGG-----AACACCCGGAGGACTCATGC 588
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 SerPheIleG1nG1nAspMetValCYsAlaG1YTrLYsG1UG1YArgIleAspAlaCYs 215

QY 589 CAGGCGACTCCGAGAGGCGCCCTGGTGTGCAAGTGAATGGCACCTGGCTGCAGCGCGGC 648
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 G1nG1YAspSerG1Yg1YPrOleuValCYsAsnValAsnAsnValTTrPleuG1nLeuG1Y 235

QY 649 GTGTGACGCTGGGGGAGGGCTGTGCCCAAGCCCAACCGGCTGGCATCTACACCGCTGC 708
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 IleValSerTTrpG1YTrCYsAlaG1nProAsnArGProG1YValTyrThrLYsVal 255

QY 709 ACCTACTTGTGAGTGCATCCACCATATGTGCC 744
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 G1nTyrTyrG1nAspTTrPleuLYsThrAsnValPro 267

```

Search completed: January 31, 2003, 06:58:26
Job time : 63.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame-plus_n2p model

Run on: January 31, 2003, 05:25:33 : Search time 17.5 Seconds
(without alignments)
3654.657 Million cell updates/sec

Title: US-09-598-982-20
Perfect score: 1458
Sequence: 1 ggagccctcgagaagaat.....cgtgaagcggccgcgctcgt 771

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODL=frame+n2p.model -DEV=xlh
-O=/cgn2_1/USPRO_pool/US09598982/unaltd_27012003_073715_19534/app_query.fasta_1.967
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -KOOCL=0
-LOOEXT=0 -UNITS=bits -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR_SCORE=1 -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982.cgn.1.1.6.urnat.27012003_073715_19534 -NCP=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGESUBJECT -NEC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARK_TIMEOUT=30 -THR_RADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELTOP=6 -DELEXT=7

Database : Swissprot_40.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	93.8	275	1	TRB2_HUMAN
2	1363	93.5	275	1	TRB1_HUMAN
3	1282	87.9	275	1	TRBA_HUMAN
4	1092	74.9	276	1	MCT6_MOUSE
5	1077	73.9	275	1	TRYT_CANFA
6	1075	73.7	270	1	TRYT_MERUN
7	1057	72.5	273	1	MCT7_MOUSE
8	1055	72.4	274	1	MCT6_RAT
9	1039	71.3	273	1	MCT7_RAT
10	1030	70.6	273	1	TRYT_SHEEP
11	1006	69.0	275	1	TRYT_PIG
12	988	67.8	235	1	TRVD_HUMAN
13	684.5	46.9	269	1	TRVM_CANFA
14	608.5	41.7	311	1	TRYG_MOUSE
15	593.5	40.7	321	1	TRYG_HUMAN
16	563.5	38.6	290	1	MRN_HUMAN
17	529	36.3	342	1	PSS8_RAT
18	526	36.1	342	1	PSS8_MOUSE

Result No.	Score	Query Match	Length	DB ID	Description
19	512	35.1	343	1	PSS8_HUMAN
20	501.5	34.4	317	1	BSS4_HUMAN
21	495	34.0	455	1	TMS5_MOUSE
22	494	33.9	314	1	TEST_HUMAN
23	476.5	32.7	324	1	TEST_MOUSE
24	474.5	32.5	454	1	TMS3_HUMAN
25	467	32.0	625	1	FALL_HUMAN
26	464	31.8	457	1	TMS5_HUMAN
27	463	31.8	306	1	BSS4_MOUSE
28	460.5	31.6	418	1	HATY_HUMAN
29	451	30.9	638	1	KAL_HUMAN
30	448	30.7	338	1	PLMN_HORSE
31	447	30.7	638	1	KAL_MOUSE
32	446.5	30.6	812	1	PLMN_BOVINE
33	445	30.5	638	1	KAL_RAT
34	444.5	30.5	271	1	EL2_RAT
35	444	30.5	333	1	PLMN_CANFA
36	443	30.4	245	1	PIRB_BOVINE
37	441	30.2	343	1	PLMN_SHEEP
38	439.5	30.1	269	1	EL2A_HUMAN
39	434	29.8	490	1	TMS2_MOUSE
40	430.5	29.5	271	1	EL2_MOUSE
41	429	29.4	810	1	PLMN_HUMAN
42	428	29.4	810	1	PLMN_MACMU
43	427	29.3	263	1	CPR2_CANFA
44	427	29.3	266	1	EL1_PIG
45	426	29.2	263	1	CTRB_HUMAN

ALIGNMENTS

RESULT 1

TRB2_HUMAN STANDARD; PRT; 275 AA.
ID TRB2_HUMAN Q9UQ17; Q9UQ16; O15664; O95827;
AC P20231; G9UQ17; Q9UQ16; O15664; O95827;
DC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE TRYPTASE beta-2 precursor (EC 3.4.21.59) (Tryptase II).
DN TP52 OR TP52.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT BETA-2).
RC TISSUE=Lung;
RX MEDLINE=90369005; PubMed=2203827;
RA Miller J.S., Moxley G., Schwartz L.B.;
RT "Cloning and characterization of a second complementary DNA for human
RT tryptase.";
RL J. Clin. Invest. 86:864-870(1990).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT BETA-2).
RX MEDLINE=93166209; PubMed=8434231;
RA Blom T., Hellman L.;
RT "Characterization of a tryptase mRNA expressed in the human basophil
RT cell line K0812.";
RL Scand. J. Immunol. 37:203-208(1993).
RN [3]
RP SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RX MEDLINE=90251647; PubMed=2187193;
RA Vanderslote P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA Caughey G.H.;
RT "Human mast cell tryptase: multiple cDNAs and genes reveal a
RT multigene serine protease family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
RN [4]
RP SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RX MEDLINE=99121069; PubMed=9920877;
RA Palladino M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT "Characterization of genes encoding known and novel human mast cell
RT tryptases on chromosome 16p13.3.";

AC Q15661; Q15663; Q9H2Y4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Trypsase beta-1 precursor (EC 3.4.21.59) (Trypsase 1) (Trypsase I).
 GN TP5B1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90251647; Pubmed=2187193;
 RA Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
 RA Caughey G.H.;
 RT "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene
 RT Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99121069; Pubmed=9920877;
 RA Pallanoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
 RT "Characterization of genes encoding known and novel human mast cell
 RT tryptases on chromosome 16p13.3".
 RL J. Biol. Chem. 274:3355-3362(1999).
 RN [3]
 RP SEQUENCE OF 54-275 FROM N.A. (ISOFORM 2).
 RA Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
 RA Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
 RA Hunt J.E.;
 RT "Molecular cloning and characterization of novel human tryptase cDNAs
 RT and splicing variants".
 RL submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROPEASE PRESENT IN MAST
 CC CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRADATION
 CC RESPONSE OF THIS CELL TYPE.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|- , Lys-|- , but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
 CC MAST CELL ACTIVATION.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
 CC -----
 CC This Swiss-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M33494; AAC8172.1; -;
 DR EMBL: M33491; AA36778.1; -;
 DR EMBL: AF09144; AAD17860.1; -;
 DR EMBL: AF206667; AAG35697.1; -;
 DR HSSP: P20231; 1A0V.
 DR MEROPS: S01.242; -;
 DR GeneW: HGNC:12019; TP5B1.
 DR MIM: 191081; -;
 DR InterPro: IPR001314; Glymotrypsin.
 DR InterPro: IPR001254; Ser_Protease_Try.
 DR Pfam: PF00089; trypsin.1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; Tryp_Spc.1.
 DR PROSITE: PS50240; TRYP_SIN_DOM.1.
 DR PROSITE: PS00134; TRYP_SIN_HIS.1.
 DR PROSITE: PS00135; TRYP_SIN_SER.1.
 DR HydroLase: Serine protease: signal; Glycoprotein; Zymogen;
 KW Alternative splicing.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 30 ACTIVATION PEPTIDE (BY SIMILARITY).

FT CHAIN 31 275 TRYPTASE BETA-1.
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM.
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 FT DISULFID 155 230 BY SIMILARITY.
 FT DISULFID 188 211 BY SIMILARITY.
 FT DISULFID 220 248 BY SIMILARITY.
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLID 79 87 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 275 AA; ADC48FDC51F37112 CRC64;
 Alignment Scores:
 Pldm. No.: 1.38e-72 Length: 275
 Score: 1363.00 Matches: 243
 Percent Similarity: 99.18% ConservatIve: 0
 Best Local Similarity: 99.18% Mismatches: 2
 Query Match: 93.48% Indels: 0
 DB: Gaps: 0
 US-09-598-982-20 (1-771) x TRB1_HUMAN (1-275)
 QY 19 ATCTGTGGGGGTCAGAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGAGTGCAGAGTC 78
 |||||||
 DB 31 IIEVALGIGLYGLINGLIALAPROARGSERLYSTRPROTPRGLVALSERILEUARGVAL 50
 QY 79 CAGGGCCCATACTGAGATGCATCTTGGCGGGGCTCCATCCACCCAGTGGGTGCTG 138
 |||||||
 DB 51 HISGLYPROTYLTPMETHISPHECYSEGLYLSERILEIENISPROGLINTRPALLEU 70
 QY 139 ACCGGCGGGCGGTGGTGGAGCCGAGTCCAGAGTCTGGCCCTCAGGGTGCAGACTG 198
 |||||||
 DB 71 TRALADALAHISCVVALDLYPROASPVALLYSASPRLEADALALAEUARGVALDINLEU 90
 QY 199 CCGGAGCAGCACCTCTACTACAGAGCACAGTCTGGCCGGTCCAGAGATCTGTCGAC 258
 |||||||
 DB 91 ARGGLUGLINHISLEUFTYTYGLINLSPRGINLEULEUPROVALSERARGDLEIIEVALHIS 110
 QY 259 CCAKAGTTCTACAGCCGCCAGATGCGAGCGGACATGCCCCCTGCGAGCGTGGAGCGCCG 318
 |||||||
 DB 111 PROGINPHELYTRHVALGLINLEGLYLAASPILEADALEUENGLINLEUENGLINLUPRO 130
 QY 319 GTGAGAGTCTCCAGGCGCACAGGCGACCGGTCACCCCGCCCTGCGAGACCTTCCCC 378
 ||| |||||||
 DB 131 VALASNVALSERSENHISVALHISTHRVALITRLEUPROVALASERGLUTRHPHEPRO 150
 QY 379 CCGGGGATGCCGTCGTCGGATCACTGGCTGGGGCGATGTGGACATGATGAGCCCTCCCA 438
 |||||||
 DB 151 PROGLYMERPROCYSTRVALITRGLYTRPGIYASPVADASPSASDGLIADARGLEUPTRO 170
 QY 439 CCGCATTTCTCTGAGCAGCGTGAAGTCCCAATATGAAACCAACATTTGTGACGCA 498
 |||||||
 DB 171 PROPPOHPHEPROLEULYGLINVALIYLSVALPROIILEMETGLIASNHISILECYASPSALPA 190
 QY 499 AAATACCAACCTTTGGCGCTTACACGGGAGAGCGAGTCCGCGATCTGCTGGAGCAGCACTGGT 558
 |||||||
 DB 191 LYSTYRHSLEGLYALITATYTRHIGLYASPSPVADARGLIEVALDARGSPSPMETLEU 210
 QY 559 TGTGCCGGGAACACCCCGGAGGAGACTCATGCCAGGGCGACTCCGGAGGGGCCCTGGTGTGC 618
 |||||||
 DB 211 CYSALAGLYASNTHRARGARGASPERCYSGINGLYASPSERGLYGLYPROLEUVALDYS 230
 QY 619 AAGTGAATGGCAGCCTGGCTGAGCGGGCGGTGTCACCTGGGGGGAAGGCGTGGCCAG 678
 |||||||
 DB 231 LYSVALASNGLYTHRTRPLEUGLINALGLYVALVALISERTTRPGYGLIYGLYCYSALAEIN 250
 QY 679 CCANACCGCCCTGGCATGTACACCCCGGTGTCACCTTCTGGATGGATGATCCACCATAT 738
 |||||||
 DB 251 PROASNAIYPROGLYITLETYTRHARGVALITRGLYTRLEUASPTRPIENHISHSITR 270
 QY 739 GTCCCGAAAAGCCG 753
 |||||||

Db 271 ValProLysPro 275

RESULT 3

TRVA_HUMAN STANDARD: PRR: 275 AA.

ID TRVA_HUMAN Q90011; Q9H2Y5;

AC P15157; Q90011; Q9H2Y5;

DT 01-APR-1990 (Rel. 14, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alpha-tryptase precursor (EC 3.4.21.59) (Trypsin 1).

GN TPST1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lung;

RX MEDLINE=90009311; PubMed=2677049;

RA Miller J.S., Westin E.H., Schwartz L.B.;

RT "Cloning and characterization of complementary DNA for human

RL tryptase.";

RL J. Clin. Invest. 84:1188-1195(1989).

RN [2]

RP REVISIONS TO 89-93 AND 108.

RA Schwartz L.B.;

RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=99121069; PubMed=9920877;

RA Pallero M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;

RT "Characterization of genes encoding known and novel human mast cell

RL tryptases on chromosome 16p13.3.";

RL J. Biol. Chem. 274:3355-3362(1999).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Lung;

RX MEDLINE=87109258; PubMed=3543004;

RA Cromlish J.A., Seidah N.G., Marcinkiewicz M., Hamelin J., Johnson D.A., Chretien M.;

RT "Human pituitary tryptase: molecular forms, NH2-terminal sequence, immunocytochemical localization, and specificity with prohormone and fluorogenic substrates.";

RL J. Biol. Chem. 265:1363-1373(1987).

CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|- , but with more restricted specificity than trypsin.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON MAST CELL ACTIVATION.

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: M30038; AAA66934.1; -

DR EMBL: AF098328; AAD17846.1; -

DR EMBL: AF206665; AAG35695.1; -

DR EMBL: AF206666; AAG35696.1; -

DR PIR: A45754; A45754.

DR HSSP: P20231.1A0L.

DR MEROPS: S01.015; -

DR MEROPS: S01.143; -

DR Genew: HGNC:12018; TPST1.

DR MIM: 191080; -

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR001254; Ser_protease_Try.

DR Pfam: PF00089; Trypsin_1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR SMART: SM00020; TRYP_SPC; 1.

DR PROSITE: PS50240; TRYPsin_DOM; 1.

DR PROSITE: PS00134; TRYPsin_HIS; 1.

DR PROSITE: PS00135; TRYPsin_SER; 1.

DR HydroLase: Serine protease; Signal; Glycoprotein; Zymogen;

KW Polymorphism: Alternative splicing.

KW SIGNAL

FT PROPEP 1 19 30

FT CHAIN 31 275

FT ACT_SITE 74 74

FT ACT_SITE 121 121

FT ACT_SITE 224 224

FT DISULFID 59 75

FT DISULFID 155 230

FT DISULFID 188 211

FT DISULFID 220 248

FT CARBOHD 132 132

FT CARBOHD 233 233

FT VARSPLIC 79 87

FT VARIANT 15 15

FT VARIANT 221 221

FT CONFLICT 215 216

FT SEQ 275 AA; 30772 MW; B9BAC4B8CB91CE75 CRC64;

Alignment Scores:

Pred. No.: 7,17e-68

Score: 1282.00

Percent Similarity: 94.69%

Best Local Similarity: 93.06%

Query Match: 87.93%

DB: 1

US-09-598-982-20 (1-771) x TRVA_HUMAN (1-275)

QY 19 ATCTGCGGGGCTCAGAGAGCCCGGCAAGAGTGGCCCTGGCAGGTGAGCTGAGACTG 78

|||||

Db 31 ILEVAlGlyGLyGLInGLInAlaIbraPrArySerIysrPrProTrPrGLInValSerIleuAryAl 50

QY 79 CAGGCGCCATFACTGGATGACACTTTCGGGGGCTCCCTCATCCAGCCCGAGTGGGTGTC 138

|||||

Db 51 ArGaSPArIqTYrTYrMethIsphecYsGLyGLySerIleuIleHISrPGLInrPValIleu 70

QY 139 ACCGGCGGCGCTGGCGGAGCCGAGAGCTCAGAGTCTGGCCGCTCAGGGTGCAC 258

|||||

Db 71 ThrAlaAlaHIScYsLeuGLyPrOAsrYAlIlySArPrLeuAlaIThrLeuAryAlGLInleu 90

QY 199 CCGGAGCAGCAGCAGCTACTTACCAGGACAGCAGCTGCGCGGTCAGGAGATTCGTGCAC 258

|||||

Db 91 ArGyGLInGLInHISleuTYrTYrGLInAsPrGLInleuPrOValSerAryGLIleValHIS 110

QY 259 CCAAGETTTACACCGCCAGATCGGAGCGGACATTCGGCCCTGGAGCTGGAGAGCGCC 318

|||||

Db 111 PrOGLInPrHeTYrIleIleGLInrGLyAlAsPrIleAlaIleuIleuIleuIleuIleuIleu 130

QY 319 GGAAGGCTCCAGCCAGCTCCAGCAGCTGACCGCTGCGCCCTGAGGAGACTTCC 378

|||||

Db 131 ValAsnIleSerSerAryValHISrThrValMetLeuPrOPrAlaISerGIuThrPrHePrO 150

65 ILeHsPrOgIntRPrVAlLeuThrAlaAlaHsCysValGlyProHIsILeLysSerPro 84
 QY 178 GCGCGCCCTCAGAGGTCACACCTCGGGAGCAGCACCCTACTACAGACCAGCAGCTGCTGCCG 237
 Db 85 GlnLeuPheAlaGValGlnLeuAlaArgGlnIleuLeuIleuLeuSer 104
 QY 238 GTCACAGACATCATCTGCTCCACCACACAGTCTTACACAGCCGCCACAGTCCAGGAGCCATCCGC 297
 Db 105 LeuAsnAlaGlnLeuAlaValHisProHisTrpHisTrpHisAlaGlnGlyAlaAspAlaAla 124
 QY 298 CTGCTGGAGCTGGAGGAGCAGCCGGTAGAGTCTCCAGCCACAGTCCACAGCCAGTCCCTGCC 357
 Db 125 LeuLeuGlnLeuGlnValAlaProValAsnValSerThrHisIleHisProIleSerIleuPro 144
 QY 358 CCGTCCCTCAGAGACCTTCCCGCCGGAGTCCCGCTGCTGGTCCAGTCCAGTCCGATG 417
 Db 145 ProAlaSerGlnThrPheProProGlyThrSerCysTrpValThrGlyTrpGlyAspIle 164
 QY 418 GACAATGATGAGCCGCTCCACCACCCGATTTCCCTGTAAGACAGAGTGAAGTCCCATTAATG 477
 Db 165 AspAsnAspGlnProLeuProProProTrpProLeuLysGlnValLysValProIleVal 184
 QY 478 GAAAACCAATTTGAGAGCAAAATACCACTTGGCGCTTACAGCGGAGAGCAGCAGTCCGC 537
 Db 185 GluAsnSerLeuCysAspArgLysTrpHisThrGlyLeuTrpGlyAspAspPhePro 204
 QY 538 ATCCGCTCCAGACATGCTGTGTGCGGGAGAACACCCGGAGGACATACCCAGGGCGGAC 597
 Db 205 IleValHisAspGlyMetLeuCysAlaGlnAsnThrArgAspSerCysGlnIleLysP 224
 QY 598 TCCGGAGGCGCCCTGCTGTCGAAGGTGAATGGACACCTGGCTGCACAGCCGGCGTGGTCCAGC 657
 Db 225 SerGlyGlyProLeuValLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 244
 QY 658 TGGGGCGAGGGCTGTGGCCAGCCACCGCCCTGGCAGTACACCCGCTGACCTACTAC 717
 Db 245 TrpGlyGlnGlyCysAlaGlnProAsnLysProGlyIleTrpThrArgValThrTrpTrp 264
 QY 718 TTGGACTGATCCACACTATGTCGCCCAAA 747
 Db 265 LeuAspTrpIleHisArgTrpValProGlu 274

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.sdb.ch).

DR EMBL: M24664; AAA30854.1; -
 DR PIR: A32410; A32410.
 DR HSSP: P20231; IMAO.
 DR MEROPS: S01.143; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_Protease_Try.
 DR Pfam: PF00089; trypsin.1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPE.1.
 DR PROSITE: PSS0240; TRYP_DOM.1.
 DR PROSITE: PS00134; TRYP_SIN_SER.1.
 DR PROSITE: PS00135; TRYP_SIN_SER.1.
 DR KW Hydroxylase; Serine protease; signal; glycoprotein; zymogen.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 31 275 TRYPASE.
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 59 75 BY SIMILARITY.
 FT DISULFID 155 230 BY SIMILARITY.
 FT DISULFID 188 211 BY SIMILARITY.
 FT DISULFID 220 248 BY SIMILARITY.
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 275 AA; C3B869251F248D5B CRC64;

Alignment Scores:
 Pred. No.: 6,13e-56 Length: 275
 Score: 1077.00 Matches: 189
 Percent Similarity: 85.71% Conservative: 21
 Best Local Similarity: 77.14% Mismatches: 35
 Query Match: 73.87% Indels: 0
 Gaps: 0

US-09-598-982-20 (1-771) x TRYP_CANFA (1-275)

QY 19 ATCGTGGGGGTCCAGAGAGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAGTCC 78
 Db 31 IleValGlnGlyAlaArgGlnAlaProGlySerLysTrpProTrpGlnValSerLeuArgLeu 50
 QY 79 CAGGCGCCATCTGAGATGACTTCTGGGGGCTCCCTCATCCACCCGCAATGGTGGTCTG 138
 Db 51 LysGlnGlnTrpTrpArgHisIleCysGlyIleSerLeuIleHisProGlnIleTrpValLeu 70
 QY 139 ACCGCGCGGGGTGGGGTGGAGCCGAGCAGTCAAGGATCTGGCCGCGCTCAGAGGTCGACCTG 198
 Db 71 ThrAlaAlaHisCysValGlyProAsnValAlaLysProGlnGlnIleArgValGlnLeu 90
 QY 199 CGGAGACAGCACCCTTACTACAGAGCAGCAGCTGCTCCGCTCAGCAGGAGATGATGCTGCAC 258
 Db 91 ArgGlnGlnHisLeuTrpTrpGlnAspHisLeuLeuProValAsnArgIleValMethHis 110
 QY 259 CCACAGTCTTACACCCGCAAGTGGAGCGGACATCCGCTGAGAGCTGGAGAGAGCCG 318
 Db 111 ProAsnTrpTrpTrpProGlnAsnGlyAlaAspIleAlaLeuLeuGlnIleAspPro 130
 QY 319 GTGAAGTCTCCAGCCAGCAGTCCACAGAGTCCAGTCCGCTGAGAGTCCAGAGCTGCC 378
 Db 131 ValAsnValSerAlaHisValGlnProValThrLeuProProAlaLeuGlnThrPhePro 150
 QY 379 CCGGGATGCGCTGCTGGCTACTGCTGGCTGGGGCGATGGAGCAATGATGAGCAGCCCTCCA 438
 Db 151 ThrGlyThrProCysTrpValThrGlyTrpGlyAspValHisSerGlyThrProLeuPro 170
 QY 439 CCGCCATTTCTTGAAGCAGGTAAGGTCGCCATTAATGAAACACCAATTTGAGAGCA 498
 Db 171 PropropPheProLeuLysGlnValLysValProIleValGlnAsnSerMetCysAspVal 190

QY 499 AANATACCCTGGGCGCTACACGGGAGACGATCCGATCGTCCGTCAGCAGATCTG 558
 Db 191 GlnTYHh1sLeuG1yLeuSerThrg1yAspRg1yValArgII1eValARg1uAspMk1eU 210
 QY 559 TGTGGCGGGAACAACCCGGGAGCAGTCATCCAGAGCCGACTCCGGAGGCCCTGGTGTGC 618
 Db 211 CysAlaG1yAsn1sSer1ySerAspSerCysG1nG1yAspSerC1yG1yPro1eUVal1Cys 230
 QY 619 AAGGTGAATGGACACCTGGTGCAGGGGGCGTGTACGCTGGGGGGGAGGGGCTGTGCCCA 678
 Db 231 ArgValArgG1yVal1TrpLeuG1nAlaG1yValValSerTrpG1yG1uG1yCysAlaG1n 250
 QY 679 CCCAACCGGCTGGCATCTACACCCGCTGTACCTACTACTGAGCTGATCCAGCAGCTAT 738
 Db 251 ProAsnArgProG1y1Le1yTrhArgValAla1Ala1yTr1yLeuAspRpr11eH1sG1n1y 270
 QY 739 GTCCCAAAAAGCCG 753
 Db 271 ValPro1ySg1uPro 275

RESULT 6
 TRYT_MERUN
 ID TRYT_MERUN STANDARD: PRT: 270 AA.
 AC P50342;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast cell tryptase precursor (EC 3.4.21.59).
 OS Meriones unguiculatus (Mongolian Jird) (Mongolian gerbil).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OC NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGS/SEA; TISSUE=Intestine;
 RX MEDLINE=95366971; PubMed=7639711;
 RA Murakumo Y, Ide H, Itoh H, Tomita M, Kobayashi T,
 RA Maruyama H, Horii Y, Nawa Y;
 RT Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil,
 RT Meriones unguiculatus, and its preferential expression in the
 RT Intestinal mucosa."
 RL Biochem J. 309:921-926(1995).
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb-sib.ch).
 CC -----
 CC EMBL: D31789; BAA06598.1;
 DR HSSP: P20231; IAAO.
 DR MEROPS: S01_143;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC_1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HTS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydroxylase; Serine protease; Signal; Glycoprotein.
 FT SIGNAL 1 25
 FT CHAIN 1 270
 FT ACT_SITE 69 69
 FT ACT_SITE 116 116
 FT ACT_SITE 219 219
 MAST_CELL_TRYPTASE.
 CHARGE_RELAY_SYSTEM (BY_SIMILARITY).
 CHARGE_RELAY_SYSTEM (BY_SIMILARITY).
 CHARGE_RELAY_SYSTEM (BY_SIMILARITY).

FT DISULFID 54 70 BY SIMILARITY.
 FT DISULFID 150 225 BY SIMILARITY.
 FT DISULFID 183 206 BY SIMILARITY.
 FT DISULFID 215 243 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 270 AA; 30166 MW; 1BE102DB86943401 CRC64;

Alignment Scores:
 Pred. No.: 8.02e-56 Length: 270
 Score: 1075.00 Matches: 188
 Percent Similarity: 84.77% Conservative: 18
 Best Local Similarity: 77.37% Mismatches: 37
 Query Match: 73.73% Indels: 0
 DB: Gaps: 0

US-09-598-982-20 (1-771) x TRYT_MERUN (1-270)

QY 19 ATGCTGGGGGTCAGAGAGCCCAAGGAGCAGATGGCCCTGGCAGGCTGAGAGTGC 78
 Db 26 11eValG1yG1nG1nG1uLa1aProG1yAsn1yTrpProTrpG1nValSer1eUArG1a 45
 QY 79 CAGGGCCATPACTGATGACATCTTGGGGGCTCCCTCATCCACCAGGAGTGTGTCG 138
 Db 46 AsnG1uTr1yTr1yParG1n1sPheCysG1yG1ySer1eU11eH1sProG1nTr1yVal1eU 65
 QY 139 ACCCGCGGCGCTGGGAGCCGAGCAGTCAAGAGTCTGGCCGCTCAGGCTGCAACTG 198
 Db 66 Th1Ala1n1h1sCysVal1d1yProTh1e1Ala1sProAsn1ySVal1ArgVal1G1n1eU 85
 QY 199 CGGAGCAGCAGCAGCTACTACACAGCAGCAGCAGCTGCTCCGTCAGCAGATCTGTCAC 258
 Db 86 Arg1ySg1n1yTr1yLeu1yTr1yTh1sAsp1s1eU1eAla1Val1Ser1Arg11e1Th1r1s 105
 QY 259 CCACAGTCTACACCGCCAGATCGGAGCGGAGCAGATCCGCTCGTGGAGCTGAGAGCCG 318
 Db 106 ProThrPheTr1yAla1ThrG1nAsnG1yAla1Asp11eAla1eU1eU1eU1ySAsnPr 125
 QY 319 GTGAAGGTCTCCAGCAGCAGCTCAGCAGGTCACCCCTGCCCTGACAGACTTGTCCC 378
 Db 126 ValAsn11eSer1eTh1sVal1h1sProVal1Ser1eUProProAla1eU1eU1eU1eU1eU 145
 QY 379 CGGGGATGCTCGCTGGGGTCACTGCTGGGGGATGTGCACAATGATGAGCCGCTCCCA 438
 Db 146 SerG1yTh1eUcysTr1yVal1ThrG1yTrpG1yAsn11eAspAsnAspVal1Ser1eUPro 165
 QY 439 CCGCCATTTCTCTGAAGGAGTGAAGTCCCAATATGAAAAACCAATTTGTGACGCA 498
 Db 166 PropRhpPro1eU1ySg1uValG1nVal1ProVal1G1nVal1G1nVal1G1nVal1eUcysAsp1eU 185
 QY 499 AANATACCCTGGGCGCTACACCCGCTGTACCTACTACTGAGCTGATCCGTCAGCAGATCTG 558
 Db 186 LysTYHh1sLeuSg1yVal1yTrhTr1yArg1yAspAsn11eH1s11eValAla1rG1yAsp1eU1eU 205
 QY 559 TGTGGCGGGAACAACCCGGGAGCAGTCATCCAGAGCCGACTCCGGAGGCCCTGGTGTGC 618
 Db 206 CysAlaG1yAsn1uG1y1h1sAspSerCysG1nG1yAspSerC1yG1yPro1eUVal1Cys 225
 QY 619 AAGGTGAATGGACACCTGGCTGCAGGGCGGCTGTGTCAGCTGGGGCGAGGGGCTGTGCCCA 678
 Db 226 LysValAsnG1yThrTr1yPLeuG1nAlaG1yVal1Val1SerTrpG1yG1uG1yCysAla1eU 245
 QY 679 CCCAACCGGCTGGCATCTACACCCGCTGTACCTACTACTGAGCTGATCCAGCAGCTAT 738
 Db 246 ProAsnArgProG1y1Le1yTrhArgVal1Th1yTr1yLeuAspRpr11eH1sArg1y 265
 QY 739 GTCCCAAAA 747
 Db 266 ValPro1yS 268

RESULT 7
 MCT7_MOUSE

ID MCT7_MOUSE STANDARD; PRT: 273 AA.
 AC 002844;
 DT 01-JUN-1993 (Rel. 26, Created)
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mast cell protease 7 precursor (EC 3.4.21.59) (MMP-7) (Trypsin).
 OS Mus musculus (Mouse).
 GN MCTP7.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090.
 RN MCTP7.
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2;
 RX MEDLINE=93087489; PubMed=1454796;
 RA McNeil H.P., Reynolds D.S., Schiller V., Ghildyal N., Gurely D.S.,
 RA Austen K.F., Stevens R.L.;
 RT "Isolation, characterization, and transcription of the gene encoding
 RT mouse mast cell protease 7."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11174-11178(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (TRUNCATED ISOFORM).
 RC STRAIN=C57BL/6J;
 RX MEDLINE=96162035; PubMed=8576265;
 RA Hunt J.E., Stevens R.L., Austen K.F., Zhang J., Xia Z.,
 RA Ghildyal N.;
 RT "Natural disruption of the mouse mast cell protease 7 gene in the
 RT C57BL/6 mouse."
 RL J. Biol. Chem. 271:2851-2855(1996).
 CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CC CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 CC RESPONSE OF THIS CELL TYPE.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
 CC truncated form; are produced by alternative splicing. The
 CC alternative splicing event is due to a G to A point mutation at
 CC the exon 2/intron 2 splice site and causes loss of protein
 CC expression. The alternatively spliced transcript is only found in
 CC C57BL/6 mouse.
 CC -1- DEVELOPMENTAL STAGE: IS NOT EXPRESSED IN MATURE SEROSAL OR
 CC MUCOSAL MAST CELLS AND IS EXPRESSED ONLY TRANSIENTLY AT AN EARLY
 CC STAGE OF IN VITRO MAST CELL DIFFERENTIATION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, TRYPTASE SUBFAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isdb-sib.ch/announce/
 CC or send an email to license@sib.ch).

FT CHAIN 29 273 MAST CELL PROTEASE 7. (BY SIMILARITY).
 FT ACT_SITE 72 72 CHANGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 119 119 CHANGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 222 222 CHANGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 57 73 BY SIMILARITY.
 FT DISULFID 153 228 BY SIMILARITY.
 FT DISULFID 186 209 BY SIMILARITY.
 FT DISULFID 218 246 BY SIMILARITY.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 44 46 VSL -> GCC (IN TRUNCATED ISOFORM).
 FT VARSPLIC 47 273 MISSING (IN TRUNCATED ISOFORM).
 SQ SEQUENCE 273 AA; 30337 MW; 50ECB475294205E CRC64;
 Alignment Scores:
 Pred. No.: 8.95e-55 Length: 273
 Score: 1057.00 Matches: 189
 Percent Similarity: 82.07% Conservative: 17
 Best Local Similarity: 75.30% Mismatches: 43
 Query Match: 72.50% Indels: 2
 Gaps: 1
 US-09-598-982-20 (1-771) x MCT7_MOUSE (1-273)
 QY 1 GGGCCCTCGAGAAAAGA-----ATCGTGGGGGTGKAGAGGCCCCGAGGAGCAATGG 54
 Db 21 GILPProAlaMetThrArgLnuGluGlyLeValGlyGlnGluAlaHisGlyAsnLysTrp 40
 QY 55 CCGTGGAGGTGAGGCTGAGAGTCCAGCGCCCAATGACTGATGCACTTGTGGGGGCTCC 114
 Db 41 ProTrpGlnValSerLeuAlaGlnAlaAsnAspThrYTrpMetHisPheCysGlyLys 60
 QY 115 STCATGCAACCCCACTGGGTGTCAGCCCGCGGCGTGGGACCGGACGGTCAAGAT 174
 Db 61 LeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProAspValAlaAsp 80
 QY 175 CTGGCGCCCTCAGGGGTGCACTGGGGGAGGAGCAACCTGCTACGAGCAGCAGCTGTG 234
 Db 81 ProAsnLysValArgValGlnLeuAlaGlnLysGlnLysLysLysLysLysLysLysLys 100
 QY 235 CCGTGCACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 294
 Db 101 ThrValSerGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
 QY 295 GCGTGGTGGAGCTGGAGGAGCGGCTGAAAGGTGCAAGCGTGCACACGGTCAACCTG 354
 Db 121 AlaLeuLeuLysLeuThrAsnProValAlaHisIleSerAspLysValHisProValProLeu 140
 QY 355 CCGCTGGCTGAGAGCACTGGGGGAGTCCCGGCGTGGCTGAGTGGGGGCGAT 414
 Db 141 ProProIaIaSerGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpIleLysn 160
 QY 415 GTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
 Db 161 IleAspAsnGlyValAlaAsnLeuProProProProProProLeuLysGlnValGlnValProIle 180
 QY 475 ATGGAAGAACCAATGTTGTGAGCAAAATAACAACCTTGGCGGCTACACGGGAGACAGCTG 534
 Db 181 IleGluAsnHisLeuCysAspLysLeuLysLysLysLysLysLysLysLysLysLysLys 200
 QY 535 CCGATGCTGGCTGAGAGCACTGGGGGAGTCCCGGCGTGGCTGAGTGGGGGAGTCCCGGCA 594
 Db 201 HisIleValAlaArgAspAspIleLeuLysAlaGlyAsnGlnGlyHisAspSerCysGlnGly 220
 QY 595 GACTCCGAGGAGGCGCTGGTGTGCAAGTGAATGGACCTGCTGCTGCTGCTGCTGCTGCTG 654
 Db 221 AspSerGlyGlyProLeuValLysLysValGlnAspThrTrpLeuGlnAlaLysValVal 240
 QY 655 ASCTGGGGGAGGAGGCTGTGTCAGCCCAAGCGGCTGGCATACACCGTGTCAACCTAC 714
 Db 241 SerTrpGlyGlnGlyCysAlaGlnProAsnArgProGlyIleLysLysLysLysLysLysLys 260
 QY 715 TACTTGGACTGGATGCACCACTATGTCGCCAAA 747

DB 261 Tyrosylserine esterase-like protein 271
 RESULT 8
 MCT6_RAT
 ID MCT6_RAT STANDARD: PRT: 274 AA.
 AC P50343; P97593;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast cell protease 6 precursor (Ec 3.4.21.59) (MCP-6) (Trypsase).
 GN MCP6 OR MCP6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal mast cells;
 RX MEDLINE=96015171; PubMed=8537314;
 RA Ide H., Itoh H., Tomita M., Murakumo Y., Kobayashi T.,
 RA Maruyama H., Osada Y., Nawa Y.,
 RT "cDNA sequencing and expression of rat mast cell tryptase";
 RL J. Biochem. 118:210-213(1995).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Peritoneal mast cells;
 RX MEDLINE=97114930; PubMed=8996238;
 RA Lutzeltschab C., Pejler G., Aveskogh M., Hellman L.,
 RA "Secretory granule proteases in rat mast cells. Cloning of 10
 RT different serine proteases and a carboxypeptidase A from various rat
 RP mast cell populations";
 RL J. Exp. Med. 185:13-29(1997).
 CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CC CELLS. AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 CC RESPONSE OF THIS CELL TYPE.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|- , Lys-|- , but
 CC with more restricted specificity than trypsin.
 CC -1- SIMILARITY: BELONGS TO TRYPTASE FAMILY SL. TRYPTASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isp.slb.ch/announce/>
 CC or send an email to license@isb.slb.ch).
 CC -----
 CC EMBL: D38455; BA07486.1; -;
 CC EMBL: U67909; ABA48262.1; -;
 CC HSSP: P20231; IAAO.
 CC MEROPE: S01.025; -;
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR001254; Ser_protease_Try.
 CC Pfam: PF00089; trypsin.1.
 CC PRINTS: PR00722; CHYMOTRYSIN.
 CC SMART: SM0020; TRY. SPEC. 1.
 CC PROSITE: PS50240; TRYPSTN_DOM: 1.
 CC PROSITE: PS00134; TRYPSTN_HIS: 1.
 CC PROSITE: PS00135; TRYPSTN_SER: 1.
 CC Hydrolyse: Serine protease; Glycoprotein; Multigene family;
 CC Signal.
 CC Signal: 1 19
 CC PROPEP 20 29 POTENTIAL.
 CC CHAIN 30 274 ACTIVATION PEPTIDE.
 CC ACT_SITE 73 73 MAST CELL PROTEASE 6.
 CC ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 223 223 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC DISULFID 58 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC DISULFID 154 229 BY SIMILARITY.
 CC DISULFID 187 210 BY SIMILARITY.
 CC DISULFID 219 247 BY SIMILARITY.
 CC CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	131	131	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	128	128	I -> N (IN REF. 2).
FT	CONFLICT	139	139	I -> T (IN REF. 2).
SC	SEQUENCE	274 AA;	30508 MW;	DP84D55668CA1A25 CRG64;

Alignment Scores:
 Pred. No.: 1.17e-54 Length: 274
 Score: 1055.00 Matches: 187
 Percent Similarity: 84.06% Conservative: 24
 Best Local Similarity: 74.50% Mismatches: 38
 Query Match: 72.36% Indels: 2
 DB: 1 Gaps: 1

US-09-598-982-20 (1-771) x MCT6_RAT (1-274)

QY	4	CCCCPCGAGAAAAG-----ATCGTCCGGGGCTGACGAGGCCSSCGGAAAGCAAGTGGCC 57
DB	23	ProvalLysGImlrValGldYlLeValGIgYlDrGulYlLaLaserGldSerGlystrPro 42
QY	58	TCGCAAGTACGCGTGCAGATCCAGCGCCCATCTGATCCACTCTGCGGGGCGTCCCTC 117
DB	43	TrpGlValSerLeuAlrGrPheLysSerPheTrMetHisPheCysGlyLysSerLeu 62
QY	118	ATPCACSSCGAGTGGGTGCCTGACSSCGCGCGCTGCTGGGAGGCGAGCAAGATCTG 177
DB	63	IleHisProGlnTrpValLeuThrAlaIleHisCysValGlyLeuHisIleLysSerPro 82
QY	178	GCGCGCGTACGGGTGACATCGTGGGAGGAGACACSTCTACTACAGAGACAGCTGCGG 237
DB	83	GluePheAlrGValGImLeuAlrGrGlnGInGInGInGInGInGInGInGInGInGIn 102
QY	238	GTACAGAGATCATCGTGCACCCAGATGTCTACCGCCGATGAGGAGAGAGATCGCGC 297
DB	103	ValAsnAlrGThrValValHisProHisIleValGlnValGlnAspGlyAlaHisPheLeu 122
QY	298	CTGTCTGAGCGTGGAGAGCGCGTGAAGTCTGCAGACAGCTGCAGACAGCTGCGCGC 357
DB	123	LeuLeuGlnLeuGlnIleIleGValAsnValSerThrHisIleHisProIleSerLeuPro 142
QY	358	CCTGCGCTAGAACCTTCCCGGCGGATGCCGCTGGTGTGACGTGGGCGGATG 417
DB	143	ProIleSerGlnThrPheProSerGlnIleHisIleHisIleHisIleHisIleHisIle 162
QY	418	GACAAATGATGACGCGCTCCACCGCATTTCTGGAAGCAGGATGAGGCTCCGCAATG 477
DB	163	AspSerAspLrProLeuAlrProLrProLrProLrProLrProLrProLrProLrProLr 182
QY	478	GAAACACATTTGTGACGSCSAAATACACACTTGGCGGCCTACACGCGAGAGCAAGTCGCG 537
DB	183	GluAsnSerLeuCysAspAlrGlyAlrGlyAlrGlyAlrGlyAlrGlyAlrGlyAlrGlyAlr 202
QY	538	ATCGTCCGTCAGACATGCTGCTGGCGGAAACACCGGAGGAGCAACTATGCCAGCGCGAC 597
DB	203	IleValGlnAspGlyMetLeuLysAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGln 222
QY	598	TCCGGAGCGCGCTGCTGCAAGGCAAGTGCACCTGCGCTGCGGAGCGCGGCTGGTGGC 657
DB	223	SerGlyGlyProLeuValLysValYValLysGlyIleTrpLeuGlnAlaLysValAsp 242
QY	658	TGGGGGAGGCGTCTGCCCGGAGCGCCGCGGAGCGGCTGCAGTACAGCGGCTGCACTATCC 717
DB	243	TrpGlyGlnGlyCysAlaGlnAlaAsnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAla 262
QY	718	TTGGACTGCATCCACCATATGCTCCCAAAAG 750
DB	263	LeuAspTrpIleHisAlrGlyAlrProGlnAlrG 273

RESULT 9
 MCT7_RAT
 ID MCT7_RAT STANDARD: PRT: 273 AA.
 AC P27435; P27436;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DR 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Trypsin,
 DE skin).
 GN MCP7 OR MCP7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RC MEDLINE=97149430; PubMed=8996238;
 RA Ludejnschab C., Pejler G., Aveskog M., Hellman L.;
 RA "Secretory granule proteases in rat mast cells. Cloning of 10
 RA different serine proteases and a carboxypeptidase A from various rat
 RA mast cell populations";
 RL J. Exp. Med. 185:13-29(1997).
 RN [2]
 RP SEQUENCE OF 29-53.
 RC STRAIN=Sprague-Dawley; TISSUE=Skin;
 RC MEDLINE=91242400; PubMed=2036367;
 RA Baganza V.J., Simmons W.H.;
 RA "Trypsin from rat skin: purification and properties";
 RL Biochemistry 30:4997-5007(1991).
 RN [3]
 RP SEQUENCE OF 29-51.
 RC TISSUE=Breast carcinoma;
 RC MEDLINE=92231826; PubMed=1314562;
 RA Eto I., Grudbs C.J.;
 RA "Separation, purification and N-terminal sequence analysis of a novel
 RA leupeptin-sensitive serine endopeptidase present in chemically
 RA induced rat mammary tumor";
 RL Biochem. J. 283:209-216(1992).
 CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CC CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 CC RESPONSE OF THIS CELL TYPE.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
 CC MAST CELL ACTIVATION.
 CC -1- TISSUE SPECIFICITY: MAST CELLS.
 CC -1- PIM: GLYCOSYLATED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL: U67910; AABA8263.1; -.
 DR PIR: A23698; A23698.
 DR PIR: S21275; S21275.
 DR HSP: P20231; IAAO.
 DR MEROPS: S01.026; -.
 DR MEROPS: S01.143; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser-_protease__try_.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRY_SPC_1.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HTS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolase: Serine protease; Glycoprotein; zymogen; signal;
 KW Multigene family.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 28 ACTIVATION PEPTIDE.
 FT CHAIN 29 73 MAST CELL PROTEASE 7.
 FT ACT_SITE 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 57 73 BY SIMILARITY.
 FT DISULFID 153 228 BY SIMILARITY.
 FT DISULFID 186 209 BY SIMILARITY.
 FT DISULFID 218 246 BY SIMILARITY.
 FT CARBOHYD 49 49 N-LINKED (GLYCNAG. . .) (PROBABLE).
 FT CONFLICT 42 42 W->V (IN REF. 3).
 FT CONFLICT 49 51 NDT->WLP (IN REF. 3).
 FT CONFLICT 51 51 NDT->WLP (IN REF. 3).
 SQ SEQUENCE 273 AA; 30400 MW; 65A5ED4D279FB284 CRC64;
 Alignment Scores:
 Pred. No.: 9.98e-54 Length: 273
 Score: 1039.00 Matches: 188
 Percent Similarity: 84.27% Conservative: 21
 Best Local Similarity: 75.81% Mismatches: 38
 Query Match: 71.26% Indels: 1
 DB: 1 Gaps: 0
 US-09-598-982-20 (1-771) x MCT7_RAT (1-273)
 QY 6 CQTGAGAAAGAAATGCGGGGGGTCAGAGGCCCCAGGAGCAATGGCCCTGGCAGGT 65
 DB 25 PTDATGGLV-GlyIleValGlyGlnGlnIleValSerGlySnlYTrpPrtGlnVa 44
 QY 66 GAGCCGAGAGTCAGCCGAGGTCATAGTGGATGCGGCGGCGCCCTCCATCCACC 125
 DB 44 lserIeunrYValAsnAspTrhYTrpMentIsphesYsgIySerIeulIeIsPr 64
 QY 126 CGATGGGCTGTCAACCCCGGGGGGCGTGGGGAGCCGCAAGATCTGGCCGCT 185
 DB 64 oIntrYValIeulThrIAlaIAlaIeIhIsCysValGIdYPrsAlAspPrAsnIyLe 84
 QY 186 CAGGTGGAACTGGGGGAGGAGCACCCTACTACCAAGCAGCAGTGTGGCGGTCAGG 245
 DB 84 uArYValGlnIleuAsnArGlySgInrYleuYTrYhIsAspHIsuIeThrValSerG1 104
 QY 246 GATCATCTGTCCAGCCAGTTCACCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCC 305
 DB 104 nIleIseerHIsPrsAspPhetYrIleAlaIAspGlyAlAspIleAlaIeulY 124
 QY 306 GCTGAGAGGAGCGGTAAGGTCCAGCCAGTCCAGCCAGTCCAGCCAGTCCGCTC 365
 DB 124 sIeuThrAsnPrsValAsnIleThrSerAsnValHIsThrValSerIeulProIAlaSe 144
 QY 366 ACAGACCTTCCCCCGGAGTCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
 DB 144 rGIuThrPherProserGlyThIleuCYstrYValIhrGlyIhrpGlyAsnIleAsnAs 164
 QY 426 TGAGGCGCTCCAGCCAGTTCCTGTGAAGCAGGTGAAGTCCCAATAGGAAACCA 485
 DB 164 rValserIeulProPrsPheProIeulGlnValGlnValProIleValGlnAsnAr 184
 QY 486 CATTTGTGACGCAAAATACACACCTTGGCGCTTACACGGGAGCAGCAGTCCGATGCTCC 545
 DB 184 gIeuCYsAspIeulYsTrYhIsIySgIYleuAsnThrGlyAspAsnValHIsIleValAr 204
 QY 546 TGAGCAGCATGCTGTGGCGGAGAACACCCGGAGAGTCAATCCAGGCGGCGACTCCGAGG 605
 DB 204 gAspAspIeulYsValIAspGlyAsnGlnGlyhIsAspserCYsGlnGlyAspSerGIYGI 224
 QY 606 GCCCCTGTGTGCAAGTCAATAGCAGCCTGCGAGCGGGGCTGTGACGCTGGGGCGA 665
 DB 224 YProIeulValCYsIySValGlnAspTrhTrpIeulInIAspIleValIAserTrpGIYGI 244
 QY 666 GGGCTGTGCCAGCCAAACCGGCGTGGGATCTACACCCGCTGCACTACTTGGAGTGG 725
 DB 244 uGIYcysAlaGlnPrsAsnArPrsGIYIleYTrhArYValIhrYTrYleuAspTr 264
 QY 726 GATTCAGCAGCATGTCGCCCAA 747
 DB 264 rIleYTrArGlyrYValPrsYs 271

RESULT 10
 TRYT_SHEEP STANDARD: PRT: 273 AA.
 AC O9XSM2:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tryptase 2 precursor (EC 3.4.21.59).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 OK NCBI_TaxID=9940;
 RN (11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Abomasum;
 RX MEDLINE=20308142; PubMed=10848900;
 RA Pemberton A.D., McAleese S.M., Huntley J.F., Collier D.D.S.,
 RA Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.;
 RA "cDNA sequence of two sheep mast cell tryptases and the differential
 RT expression of tryptase and sheep mast cell proteinase-1 in lung,
 RT dermis and gastrointestinal tract";
 RL Clin. Exp. Allergy 30:818-832(2000).
 CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CC CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 CC RESPONSE OF THIS CELL TYPE.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|- , Lys-|- , but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: HOMOTETRAMER (By Similarity).
 CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
 CC MAST CELL ACTIVATION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, TRYPTASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib.ch).

US-09-598-982-20 (1-771) x TRYT_SHEEP (1-273)
 QY 19 ATCTGTCGGGGGTCAGAGGGCCCGCCAGGAGCAGTGGCCCTGGCAGTGCAGAGTC 78
 Db 29 LLEIIEGLYGLYLSGLDYLALPRGLYSERARGTRPRGTRPRGLVALSERLEUVALYL 48
 QY 79 CAGGGCCCATCTAGTGCATCTTCTGCGGGGGGCTCCATCCACCCCGCAGTGGCTGTG 138
 Db 49 ARGARGLNLTGTRARGHISGLINDYSGLYLSERLEUVALSERLEUVALSERLEUVAL 68
 QY 139 ACCGGCCGGGCGCTGGCTGGGAGCCGAGCAGTCAAGATCTGGCCGCGCTCAAGGCTG 198
 Db 69 FHLALALANISCSYLIEDLYPROGLULENGINGLIPROSERASPRHEARGVALGINDLEU 88
 QY 199 CCGGAGACAGCAGTCTAGTACAGAGCCAGTCCAGTCCGCTGGCTGGAGAGATCTGTCG 258
 Db 89 ARGGLINGLNIHLEUPLYRGLINSPARGYLEUVALSERARGVALILEPROHIS 108
 QY 259 CCACAGTCTACACCCGAGATCGAGCCGAGCCGATCCGCTGGAGCTGGAGGAGCCG 318
 Db 109 PRONHISTYTRTYMETVALGIDUANSGLYALASPRILEALALEUDELINDLEUVAL 128
 QY 319 GTGAAGTCTCCAGCCAGTCCAGCAGCCAGTCCAGCCGCTGGCCGAGAGCCTTCC 378
 Db 129 VALSERLESERARGHISVALGINDPROVALTRHLEUVALSERGLVTRHPRHPR 148
 QY 379 CCGGGAGTCCGCTGGCTGGTCACTGGCTGGGCGCATGTGGACAAATGATGAGCCCTCC 438
 Db 149 PROGLUSERGLCSYRPRVALRHRGLYRGLYASRVALASPARISGLYARPRGTRPR 168
 QY 439 CCGCCATCTCTCTGTAAGGAGGTGAAGGTCGCCAATGAAAGCAATGTTGTGACGCA 498
 Db 169 PROPRGTYRPRGLEYLGLINDVALYLSVALPROLLEVALGIDANSERVALYLSASPT 188
 QY 499 AATATCCACCTGGCGGCTGACAGGAGAGCAGTCCGCTGGCTGGAGCAGCAGTCTG 558
 Db 189 LYSYLNHISERGLYLEUSERTHRSPRYSERVALPROLLEVALGINDUANSPLANSLEU 208
 QY 559 TGTGCGGGGADACCCCGGAGGAGCATATCCAGGCGGAGTCCGGGAGGCGCCCTGGTGC 618
 Db 209 CYSALAGLYASRGLYGLYARGLASPSERYCSGLNGLYASPSERGLYLPYRLEUVALCY 228
 QY 619 AAGGTGAATGGACAGTGGCTGAGGCGGCGGTGTCAGTGGGAGGCGGCTGTGGCCAG 678
 Db 229 LYSVALASRGLYTRHTRPRLDGLNLAGLYVALVALSERTRPGLYASRGLYCSALAT 248
 QY 679 CCCAACCCGCGCTGGCATCTACACCCGCTGTCCACTACTGTGAGTGCAGCAGCATAT 738
 Db 249 PROASNARGPRGGLYLETYRTHRARGYLIERHSERYTLEUASPRYRLEHISGLIN 268
 QY 739 GTGCCCAAAAAGCCG 753
 Db 269 VALPRGGLINGLIPRO 273

RESULT 11
 TRYT_PIG STANDARD: PRT: 275 AA.
 AC O9N2D1:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Tryptase precursor (EC 3.4.21.59).
 GN MCT7.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 CC NCBI_TaxID=9823;
 RN (11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=20285343; PubMed=10824103;
 RA Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,

FT CARBOHYD 95 95 N-LINKED (GLCNAc...) (POTENTIAL)
 FT CARBOHYD 106 106 N-LINKED (GLCNAc...) (POTENTIAL)
 SQ SEQUENCE 269 AA; 29824 MW; BA4A4F7EA82FDD4E5 CRC64;

Alignment Scores:
 Pred. No.: 4.29e-33 Length: 269
 Score: 684.50 Matches: 132
 Percent Similarity: 65.34% Conservatve: 32
 Best Local Similarity: 52.59% Mismatches: 78
 Query Match: 46.95% Indels: 9
 Gaps: 1 4

US-09-598-982-20 (1-771) x TRYX_MOUSE (1-269)

```

QY 19 ATCTGGGGGGGTCAGAGAGGGCCGCGAGAGCAAGTGGCCCTGGCAGGTGAGAGTTC 78
    |||||
Db 20 lIevAlGlYgLyCysLyVAlPrOlAhrAgYrPrOTRPrGlVAlSerLeuAhrPrhE 39
QY 79 CAGGCG-----CQAFTGGATGCACTTTCGCGGGGGTCCCTCATCCAGCCCCAG 129
    |||||
Db 40 HSlGlyMeTGlYserGlYGlNTrPrGlNHSlIecYsGlYglYserLeuIHSlPrOgIn 59
QY 130 TGGGGTCAGCCGGGGGGCGGCGGAGCCGAGCCGACGGTCAAGATCTGGCCCGCCAGG 189
    |||||
Db 60 TrVAlLeuTHrAlAlAlhSlcYsVAlGlYleuGlYlAlAlAlAhrLeuAhrG 79
QY 190 GTGCAACTGGCCGAGCAGCACTTACTACTACAGCAAGCAGCAGCTCCCTGCAGAGATC 249
    |||||
Db 80 ValGlNValGlYglYleuAlrYleuAhrYrAhrPrhSlAsPrGlNleuCysAsnVAlNhrGlUlE 99
QY 250 ATCTGGTACCCAGTTCATACAGCCGCCAGATCGA-----GGCAATCGCCCTG 300
    |||||
Db 100 lIeAlrGlNlSPrOlAhrPrhEAsnMeTserTrYrGlYTrPrASPrTHrAlAlSPrIleAlLeu 119
QY 301 CTGGAGTCAGAGGAGCGGGTCCAGAGTTCAGCAGCAAGTTCAGCAGGTCAGCCCGCCT 360
    |||||
Db 120 LeuYlSleuGlNAlArPrOlAhrLeuHrLeuSerGlYAsrVAlAlNleuVAlSerLeuPrOser 139
QY 361 GCTTGTGAGAGACTTCCGCCGGAGTCCGCTGGTCTACTCTGGTGGCGCATGTGGAC 420
    |||||
Db 140 PrOserLeuIHleVAlPrOserPrOserPrOserPrOserPrOserPrOserPrOserPrOser 159
QY 421 AATGATGAGGGCTCCGAGCAGCGCGCATTTCTCTGTGAAGGATGAGGTCCCGAATATGGA 480
    |||||
Db 160 AsrNlSPrHrPrOserPrOserPrOserPrOserPrOserPrOserPrOserPrOserPrOser 179
QY 481 AATGCATTTGGAGCGCAAAATATACCACTTTGGCGCTTACAGCGGAGAGAGAGCGCCGATC 540
    |||||
Db 180 AsnAlrGlYlCysAsnYhSlhSlYrGln-----THrIHleuGlUelNhrSPrGlVAl 197
QY 541 GTCGCTGTGAGCAGATGCTGTGTGCGGGGAGAGCAGCGGAGAGACTCAGTCCAGGCGCATCC 600
    |||||
Db 198 lIeYlSlnAsPrMeTleuYsAlrGlyserGlYglYhNlAsPrSerCyslNMeTAsPrSer 217
QY 601 GAGAGGGGGGGCTGTGGCAAGGTGAAGTGGACAGTCCGCTGCAGGCGGCTGGTGGTGG 660
    |||||
Db 218 GlYglYPrOleuVAlCysAhrYrPrYlSPrYsCysrThrPrIleGlNValAlYVAlAlSerTr 237
QY 661 GGGGAGGGGGTGTGGCCAGCGCAAGCGGCGGCTGGAGCTTACAGCGGAGAGCTGACTGACT 720
    |||||
Db 238 GlYTrGlYglYCysGlYTr-----AsnLeuPrOglYVAlTrYAlArYVAlAhrSerTrYVAl 256
QY 721 GACTGTGATTCAGCACTATGCTCCCAAAAAGCCG 753
Db 257 serTrPrIHSlSlnlIerPrOleuSerPro 267
    
```

Alignment Scores:
 Pred. No.: 1.13e-28 Length: 311
 Score: 608.50 Matches: 123
 Percent Similarity: 60.63% Conservatve: 81
 Best Local Similarity: 48.43% Mismatches: 81
 Query Match: 41.74% Indels: 19
 Gaps: 1 6

US-09-598-982-20 (1-771) x TRYX_MOUSE (1-311)

```

Db 16 AGAATGTGCGGGGGTCAGAGAGGGCCGCGAGAGCAAGTGGCCCTGGCAGGTGAGAGTTC 75
    |||||
Db 29 ArgIHleVAlGlYglYhNlSlnAlArPrOlAhrYlTrPrPrOglNlAsPrLeuAhrG 48
    
```

DE TrypTase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
 GN TPSS1 OR TWI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv. and BALB/C;
 RA Medline=99452974; PubMed=10521469;
 RA Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
 RA Friend D.S., Krill S.A., Stevens R.L.;
 RA "Identification of a new member of the tryptase family of mouse and
 RA human mast cell proteases which possesses a novel COOH-terminal
 RA hydrophobic extension."
 RL J. Biol. Chem. 274:30784-30793 (1999).
 CC -i- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
 CC -i- TISSUE SPECIFICITY: Expressed in many tissues.
 CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
 CC -i- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC of the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF175760; AAF03698.1; -;
 DR EMBL: AF175523; AAF03696.1; -;
 DR HSSP: P20231; IAAO. -;
 DR MEROPS: S01.028; -;
 DR MGD: MGI:1349391; Tpsgl.
 DR InterPro: IPR001314; Chymotrypsin.
 DR Pfam: PF00089; trypsin.1
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP-SPC.1.
 DR PROSITE: PS50240; TRYP_SIN_DOM.1.
 DR PROSITE: PS00134; TRYP_SIN_HIS.1.
 DR PROSITE: PS00135; TRYP_SIN_SER.1.
 KM Hydroxylase: Serine protease; Signal; Glycoprotein; Zymogen;
 KM Transmembrane. 1
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 28 TRYPTASE GAMMA LIGHT CHAIN.
 FT TRANSMEM 30 311 TRYPTASE GAMMA HEAVY CHAIN.
 FT ACT_SITE 277 297 POTENTIAL.
 FT ACT_SITE 70 70 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 117 117 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 18 18 INTERCHAIN (POTENTIAL).
 FT DISULFID 55 71 BY SIMILARITY.
 FT DISULFID 151 220 BY SIMILARITY.
 FT DISULFID 184 202 BY SIMILARITY.
 FT DISULFID 210 238 BY SIMILARITY.
 FT CARBOHYD 77 77 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 311 AA; 32656 MW; 7FC9D6E6FA2A8808 CRC64;

```

OY 76 GTCACGGCCCATCTAGTGCATCTTCCGGGGGCTCCCTCATCCACCCCGAGTGGTGG 135
    :::::||||| |||||||||||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 49 LeuH1Lys-----ValHisValCysGlySerLeuLeuSerProbiLurPrVal 65
OY 136 CTGACCCCGCCCGCGTGGTGGGACCGGACGTCAAGATCTGGCCCGCTCAGGGTCAA 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 LeuThrAlaAlaHisCysPheSerGlySerValAsnSer-----SerAspTrpAlaHis 84
OY 196 CTGGGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 LeuGlyGlyLeuThrValThrLeuSerProHisPheSerThrValLysTrpGlyLeuMet 104
OY 256 CACCCACAGTCTACACCCGCCAGATCCGGA-----GCGCACATCCGCCCTG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 105 -----TyrThrGlySerProGlyProGlySerGlyLysPheAlaLeu 120
OY 301 CTGACAGCTGGAGGACCGGTGAAGTCTCCACGACGTCACACGCTCACCCCTGCCCT 360
    :::::||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ValGlnLeuSerSerProValAlaLeuSerSerGlnValGlnProValCysLeuProGln 140
OY 361 GCCTCAGACAGCCTTCCCTCCCGGGGATGCCGCTGGTGCATGGGCGGCGCATGTGGAC 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 AlaSerAlaAspPheTyrProGlyMetGlnCysTrpValThrGlyTrpGlyThrGly 160
OY 421 AATGATGAGCGCCCTCCACCCGCTCCCTCAAGACAGGTGAAGGTCCTCCCATATGAA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 GluGlyGlnProLeuLysProProGlyTrpAsnLeuGlnGlnAlaLysValSerValValAsp 180
OY 481 AACCAATTGTGACGGCAAAATRACACCTTGGCGCTACAGCGGAGACAGCAGCTCCGCAATC 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 ValLysThrCysSerGln-----AlaTyrAsnSerProAsnGlySerLeu 195
OY 541 GTCGCGGACGAGATGCTGTGGCGGGGAAACACCGGAGGAGGAGCAGCGGCGGCTCC 600
    :::::||||| ||||||||||||| ||||| ||||| ||||| ||||| |||||
Db 196 IleglnProAspMetLeuGlySalaArgGlyPro--GlyAspAlaCysGlnAspSpp 214
OY 601 GGAGGGCCCTGTGTGCAAGTGAATGGCACCTGGCTCCAGCGCGCGCTGTGACGTGG 660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 215 GlyGlyProLeuValCysGlnValAlaGlyTrpGlnAlaGlyValValSerTrp 234
OY 661 GCGGAGGCTGTGCCCGCCACCGGCGCTGGCATCTACCCCGTGTCACTACTGTGG 720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 GlyGlyGlyCysGlyAspGlyProAspArgProGlyValLysValAlaArgValThrAlaTyrVal 254
OY 721 GACTGGATCCACTATGTCCCAAAAAGCCGTTGAAGGGG 762
    :::||||| |||||||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 255 AsnTrpIleHisHisHisIleProGluAlaGlyGlySerGly 268

```

```

RA Friend D.S., Krilis S.A., Stevens R.L.;
RT "Identification of a new member of the tryptase family of mouse and
RT human mast cell proteases which possesses a novel COOH-terminal
RT hydrophobic extension."
RN J. Biol. Chem. 274:30784-30793(1999).
RN [3]
RA SEQUENCE OF 220-321 FROM N.A.
RP Mitten S., Agnew W.S.;
RT "Organization and alternative splicing of CACNA1H.";
RL Submitted (Jan-2001) to the EMBL/Genbank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
CC -I- TISSUE SPECIFICITY: Expressed in many tissues.
CC -I- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
CC differ by 5 residues.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; AF191031; AAF76457.1; -
DR EMBL; AF195508; AAF76458.1; -
DR EMBL; AF175759; AAF03697.1; -
DR EMBL; AF175522; AAF03695.1; -
DR EMBL; AF225563; AAG48852.2; -
DR HSPD; P00763; IDPO.
DR MEROPS; S01.028; -.
DR Genew; HGNC:14134; TPST1.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser__protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSTN_DOM; 1.
DR PROSITE; PS00134; TRYPSTN_HIS; 1.
DR PROSITE; PS00135; TRYPSTN_SER; FALSE_NEG.
KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Transmembrane; Polymorphism.
FT SIGNAL 1 19
FT CHAIN 20 36
FT TRANSMEM 38 321
FT ACT_SITE 284 304
FT ACT_SITE 78 78
FT ACT_SITE 125 125
FT ACT_SITE 222 222
FT DISULFID 26 26
FT DISULFID 63 79
FT DISULFID 159 228
FT DISULFID 192 210
FT DISULFID 218 246
FT CARBOHYD 85 85
FT VARIANT 60 60
FT VARIANT 126 126
FT VARIANT 132 132
FT VARIANT 204 204
FT VARIANT 288 288
FT CONFLICT 160 160
FT SEQUENCE 321 AA; 33827 MW; FFF7B06E3C4A952D CRC64;

```

Alignment Scores:
 Pred. No.: 8.39e-28
 Score: 593.50
 Percent Similarity: 61.89%
 Best Local Similarity: 48.77%

Query Match: 40.71% Indels: 13
 DB: 1 Gaps: 6

```

US-09-598-982-20 (1-771) x TRYG_HUMAN (1-321)
OY 16 AGAATCGTGGGGGTGACAGGAGCCGACAGCAAGTGGCCSTGGACAGTGGACCTGAGG 75
   |||||
Db 37 ArgIleValIGIYGIYIAlaIValnIAlaIArgIValatIArgIValatIArgIValatI 56
OY 76 GTCACAGGSSCATACTGATGACACTTTCGCGGGGCTCCCTGATCCACCCCAATGGGGT 135
   |||||
Db 57 LeuArgIArg-----MethIValCysGIYGIYSerLeuLeuSerProGIInIrrVal 73
OY 136 CTGACCCGCGGGGCTGGTGGAGCCGACGCAAGGATCTGGCCCTCCAGGGTGCDA 195
   |||||
Db 74 LeuIrrIAlaIAlaIAlaIHisCysIrrPheSerGIYSerLeuAnsSer----SerAsp 92
OY 196 CTGGCGGAGACAGCACTCTACTACAGGACCACTGCTGGCCGCTGACGACATCTCTG 255
   |||||
Db 93 LeuGIYGIYLeuGIYIleIrrIrrLeuSerProIHisPheSerThIrrValIArgIInI 112
OY 256 CACCCACAGTTCATACAGCCGACAGTTCGGA-----GCGGACATCCGCTCTGGAGCT 309
   |||||
Db 113 HisSerSer--ProSerGIYInProGIYIrrSerGIYAspIleAlaLeuValIGIYLeu 131
OY 310 GAGGAGCCGCTGAAGGCTCTCCAGCCAGCTCCACAGGCTCACCCCTCCCTCCAGAG 369
   |||||
Db 132 SerValIrrValIrrLeuSerSerArgIleIrrProValCysLeuProGIInIrrSer 151
OY 370 ACCTTCCCGCGGGGATGGCCGTGGTGGTCACTGGCTGGGGGATGGACAAATGATGAG 429
   |||||
Db 152 AspIrrPheCysIrrGIYIleIrrGIYIrrValIrrGIYIrrGIYIrrGIYIrrGIYI 171
OY 430 CGCCCTCCAGCCGCTCATTCCTCTGAAGCAGTGAAGGTCACCATTAATGGAAACCAAT 489
   |||||
Db 172 ProLeuProIrrProIrrIrrSerIrrLeuIrrGIYValIrrValSerValIrrVal 191
OY 490 TGTGACGGCAAAATACACACCTTGGCCCTTACACAGGAGACGACGTCGCCGATGCC 549
   |||||
Db 192 CysArgIrrArgAsp-----TyrProGIYProGIYSerIrrLeuGIInIrrPro 206
OY 550 GACATGCTGTGTGGCCGGGAAACACCCGGAGGAGACTCATGCGGAGGACTCCGGAGGCCC 609
   |||||
Db 207 AspMetIrrCysIrrAlaIrrGIYIrrPro--GIYAspIrrAlaCysIrrAspSerGIY 225
OY 610 CTGGTGTGCAGAGTGAATGGCACTGGCTGGCTGCAGGGGGGCTGGTCAAGTGGGGCC 669
   |||||
Db 226 LeuValCysGIYValnIrrValnIrrValnIrrValnIrrValnIrrValnIrrValn 245
OY 670 TGTGGCCAGCCGACCCGCTGGATCTACACCCGCTGACCCGCTGACCTACTACTACT 729
   |||||
Db 246 CysGIYArgIrrProAsnIrrArgIrrProGIYValIrrGIYIrrIrrValIrrVal 265
OY 730 CACCACTATGTC 741
   |||||
Db 266 ArgArgHisIle 269
    
```

Search completed: January 31, 2003, 06:54:08
 Job time : 34.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2003, 06:53:20 ; Search time 16.5 Seconds
(without alignments)
2749.706 Million cell updates/sec

Title: US-09-598-982-20
Perfict score: 1458
Sequence: 1 ggagccctcgagaagaat.....cgtgaagcggccgctcgt 771

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command Line parameters:
-MODBL=frame+n2p.model -DEV=xlh
-Q=/cgn2_1/USPNO_spool/US09598982/runat_27012003_073718_19604/app_query.fasta_1.967
-DB=Issued_Patents_AA -QPMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsm62 -TRANS=human40.cdd
-LIST=45 -DOCCALIGN=200 -THR_SCORE=DCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982 @CGN_1_1_4 @runat_27012003_073718_19604 -NCPU=6 -ICPU=3
-NO_XLPPY -NO_LMAP -LARGESUBSTR -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEROUT=120
-WARN_TIMEROUT=30 -THRADSD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCtus.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1387	95.1	249	4	US-09-079-970A-5
2	1368	93.8	245	4	US-09-079-970A-6
3	1368	93.8	274	2	US-09-016-366A-21
4	1368	93.8	274	2	US-08-978-404B-16
5	1363	93.5	273	2	US-09-016-366A-19
6	1363	93.5	273	2	US-08-978-404B-14
7	1344	92.2	267	2	US-09-016-366A-23
8	1344	92.2	267	2	US-08-978-404B-18
9	1274	87.4	245	4	US-08-944-483-69
10	1274	87.4	275	2	US-09-016-366A-17
11	1274	87.4	275	2	US-08-978-404B-12
12	1092	74.9	276	2	US-09-016-366A-15

13	1092	74.9	276	2	US-08-978-404B-21	Sequence 21, Appl
14	1075	73.7	270	2	US-08-978-404B-8	Sequence 8, Appl
15	1057	72.5	273	2	US-08-978-404B-3	Sequence 3, Appl
16	1055	72.4	274	2	US-08-978-404B-5	Sequence 5, Appl
17	1039	71.3	273	2	US-08-978-404B-6	Sequence 6, Appl
18	702	48.1	190	2	US-08-845-998-4	Sequence 4, Appl
19	702	48.1	190	4	US-09-206-537-4	Sequence 4, Appl
20	702	48.1	190	4	US-09-430-854-4	Sequence 4, Appl
21	698	47.9	190	2	US-08-845-998-6	Sequence 6, Appl
22	698	47.9	190	4	US-09-206-537-6	Sequence 6, Appl
23	698	47.9	190	4	US-09-430-854-6	Sequence 6, Appl
24	684.5	46.9	269	2	US-08-978-404B-10	Sequence 10, Appl
25	663.5	38.6	290	4	US-09-386-653A-7	Sequence 7, Appl
26	554.5	38.0	315	4	US-09-386-653A-9	Sequence 9, Appl
27	507	34.8	319	4	US-09-386-642-12	Sequence 12, Appl
28	507	34.8	328	4	US-09-386-642-11	Sequence 11, Appl
29	506	34.7	299	4	US-08-944-483-66	Sequence 66, Appl
30	501.5	34.4	317	4	US-09-386-629-7	Sequence 7, Appl
31	494	33.9	314	4	US-09-008-271A-3	Sequence 3, Appl
32	492.5	33.8	327	4	US-09-386-629-8	Sequence 8, Appl
33	480.5	33.0	306	4	US-09-386-642-53	Sequence 53, Appl
34	476	32.6	454	4	US-09-518-046-2	Sequence 2, Appl
35	460.5	31.6	418	1	US-08-508-448C-25	Sequence 25, Appl
36	460.5	31.6	418	4	US-09-370-838-82	Sequence 82, Appl
37	460.5	31.6	418	4	US-09-370-838-83	Sequence 83, Appl
38	460	31.6	238	4	US-08-944-483-64	Sequence 64, Appl
39	458.5	31.4	418	4	US-09-370-838-62	Sequence 62, Appl
40	449.5	30.8	232	1	US-08-508-448C-19	Sequence 19, Appl
41	446	30.6	248	4	US-08-944-483-63	Sequence 63, Appl
42	445	30.5	638	2	US-08-681-151-3	Sequence 3, Appl
43	431.5	29.6	241	1	US-08-944-483-59	Sequence 59, Appl
44	431	29.6	791	1	US-08-643-219-1	Sequence 1, Appl
45	431	29.6	791	3	US-08-851-350-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-079-970A-5
; Sequence 5, Application US/09079970A
; Patent No. 6274366
; GENERAL INFORMATION:
; APPLICANT: Mafilt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Fructase and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079, 970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506, 073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO.: 5:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-079-970A-5

```

```

Alignment Scores:
Pred. No.: 1.5e-104 Length: 249
Score: 1387.00 Matches: 248
Percent Similarity: 99.60% Conservat: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 95.13% Indels: 0
DB: Gaps: 0

```

US-09-598-982-20 (1-771) x US-09-079-970A-5 (1-249)

```

OY 7 CTCGGAAGAAAGATGCTGGGGGTTAGGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTC
Db 1 LeuGIuLysArgIleValGIgLIgLIuAlaProAlaArgSerLysTrpProTrpGIuVal
OY 67 AGCCGAGAGTCCAGCCGCGCCATACGATGAGTCACTTCGGGGGGCTCCCTCATCCAGCCC
Db 21 SerLeuAlaGValHisGILyPrOlyTrpMetHisPheCysGLyLysSerLeuIleHisPro
OY 127 CAGTGGTGTGACCCCGCCGCGCTGCGTGGGAGCCGACGTCAGAGATCTGGCCCGCTC
Db 41 GIuTrpValIleuThrAlaAlaHisCysValGIyTrpAlaSerValLysAspLeuAlaIleu
OY 187 AGGCTGCACATGCGGGAGCAGCAGCCTGTACTACACAGACCCAGCAGCAGCCTGCGGTCAGCAGG
Db 61 ArgValGIuLeuArgGIuGIuHisIleuTyTrpGIuAspGIuLeuLeuProValSerArg
OY 247 ATCATGCTGCACCCGACATGCTGTACACCGCCGACATGCGGAGGAGGAGATGCGCTGGTGGAG
Db 81 IleIleValHisPheGluIlePheTyThrAlaGluIleGIuAlaAspIleLeuLeuGIu
OY 307 CTGAGGAGCCGCGTGAAGGCTGTCCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
Db 101 LeuGIuGIuProValLysValIleSerHisValHisIleTrpValIleuProProAlaSer
OY 367 GAGACCTTCCCGCCGGGATGCGCTGGTCACTGGCTGGGCGGATGTGGACAATGAT
Db 121 GIuTrpIlePheProGIuMetPheProCysTrpValIleTrpGIuLysValAspAlaAspAsnAsp
OY 427 GAGGCGCTCCCGCCGATTCCTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
Db 141 GIuAlaGluProIleProIlePheProLeuLysGIuValLysValIleuIleMetGIuAsnHis
OY 487 ATTTGTGACGCAAAATACCACTTGGCCGCTTACACGCGGAGCAGCAGCAGCAGCAGCAGCAGC
Db 161 IleCysAspAlaLysTrpHisIleuGIuLysIleTrpGIuAspAspValAlaArgIleValAlaArg
OY 547 GACGACATGCTGTGTCGGGGGAAACACCCGGAGGAGCTATGCGCAAGGGGAGCTCCGGAGGG
Db 181 AspAspMetLeuCysAlaGIuLysnIleTrpArgAspSerCysGIuGIuLysPheSerIleGIu
OY 607 CCCCAGTGTGCAGGAGTGAATGGCACTGGGCGTGGAGGCGGCGGCTGAGGCTGGGGGGGAGG
Db 201 ProLysValIleCysLysValAsnGIuLysTrpLysGluAlaGIuValIleValIleSerTrpIleGIu
OY 667 GCGTGTGCGCCAGCCAGCCAGCCGCTGGCATCTACACCCGCTGACCTACTACTGGAGCTGG
Db 221 GIuCysAlaGIuProAlaAsnArgProGIuLysIleTrpIleArgValIleThrTyTrpLeuAspTrp
OY 727 ATCCACGACATGCTCCCAAAAAGCCG 753
Db 241 IleHisHisTyValIleProLysLysPro 249

```

```

; APPLICANT: Maffitt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Trypsin and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079, 970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506.073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-079-970A-6
Alignment Scores:
Pred. No.: 5.12e-103 Length: 245
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservat: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 93.83% Indels: 0
DB: Gaps: 0
US-09-598-982-20 (1-771) x US-09-079-970A-6 (1-245)
OY 19 ATGCTGGGGGTTCAAGGAGCCCGCCAGAGCAAGTGGCCCTGGCAGGTCGAGAGTC 78
Db 1 IleValGIuGIuGIuAlaIleProAlaArgSerLysTrpProTrpGIuValIleSerLeuAlaArgVal
OY 79 CAGCGCCGATACGATGACATGCTTGGCGGGGCTCCGTCACACCCAGGAGGCTGGCTG 138
Db 21 HisGIuProTyTrpMetHisPheCysGLyLysSerLeuIleHisPheGluIleTrpValIleu
OY 139 ACCGCGCGCGCTGGCGGAGCCGAGCAGTCAAGATCTGGCCGCTGAGGCTGCAAGTCG 198
Db 41 ThrAlaIleHisCysValGIyTrpAlaSerValLysAspLeuAlaIleValIleuAlaArgValGIuLeu
OY 199 CCGGAGCAGCAGCCTTACTACAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
Db 61 ArgGIuGIuHisLeuTyTrpGIuAspGIuIleuLeuProValIleSerArgIleIleValHis
OY 259 CCACAGTCTGTACACCCGCGCCAGATGCGGCGGAGCATGCGCCGCTGGAGCTGGAGGAGCCG 318
Db 81 ProGIuIlePheTyTrpIleGIuIleGIuAlaAspIleAlaLeuIleGIuIleuGIuIleuGIuPro
OY 319 GTGAGGCTTCCAGCCAGCAGCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
Db 101 ValLysValIleSerHisValHisIleThrValIleTrpProAlaIleSerGIuIleHisPhePro
OY 379 CCGGAGATGCGCTGGCTGCTACTGCTGGGCGGCTGGGCGGATGTGACAAATGATGAGCCCTCCCA 438

```


Db 121 ProGIyMePrOCySTrYrValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 140
 QY 439 CCGCCATTTCCTGTGAGCAGGTGAAGGTCGCCATTAATGGAACCAACCATTTGTGACGCA 498
 Db 141 ProPrOPhePrOleuLysGlnValLysValProIleMeGluAsnHisIleCysAspAla 160
 QY 499 AAATACACACCTTGGCCCTTACACGGGAGAGACGTCGCCATCGCTCCGTGACGACATGCTG 558
 Db 161 LysTyrHisLeuGlyAlaLeuTyrThrGlyAspAspValArgIleValIArgAspAspMetLeu 180
 QY 559 TGTGGCGGGAACACCCGGAGGACATCATGCGACGGGCGACTCCGGAGGGCCCTGGTGTGC 618
 Db 181 CysAlaGlyAsnTrpThrArgTrpAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 200
 QY 619 AAGGTGAATGGACACCTGGCTGAGGGGGCGTGCAGCTGGGGGGGAGGGGCGTGGCCGAC 678
 Db 201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 220
 QY 679 CCCAACGGGCTGGGATCTTACACCCGCTGTACACCTACTACTGACTGACTGATCCACCACTAT 738
 Db 221 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 240
 QY 739 GTCCCAAAAACCCG 753
 Db 241 ValProLysLysPro 245

RESULT 3

US-09-016-366A-21
 ; Sequence 21, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TIME OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ. ID NO.: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 274 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-016-366A-21
 ; Alignment Scores: 5.25e-103 Length: 274
 ; Pred. No.:

Score: 1368.00 Matches: 244
 Percent Similarity: 99.59% Conservation: 0
 Best Local Similarity: 99.59% Mismatch: 1
 Query Match: 93.83% Indels: 0
 DB: 2 Gaps: 0

US-09-598-982-20 (1-771) x US-09-016-366A-21 (1-274)

QY 19 ATGTCGTCGGGGGTCAGAGGGCCCGCCAGAGACAGTGGCCCTGGCAGGTGACCTGAGAGTC 78
 Db 30 LLevalGlyGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuIlyVal 49
 QY 79 CAGGCGCCATTAAGTATGATGACATTTGCGGGGGCGCTCCATGACCCCGCATGAGGTGCG 138
 Db 50 HisGlyProTyrTrpMethIAspCysGlyGlySerLeuIleHisProGlnTrpValLeu 69
 QY 139 ACCGGCGCGCGCTGGCTGGGAGCCGGACGTCAAGATGTCGGCCCTGACGGGTGCAACTG 198
 Db 70 ThrAlaIleHisCysValGlyProAspValLysAspLeuAlaIleValArgValGlnLeu 89
 QY 199 CCGGAGACACACCTTACTACAGAGACAGACAGTCCGCTGGCGTGGAGAGATCATCGTGCAC 258
 Db 90 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 109
 QY 259 CCACAGTTCCTACACCGCCAGATCGAGCGGAGCGGACATCGCCCTGGAGCTGGAGAGCCG 318
 Db 110 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlnIleGlnIleGlnIle 129
 QY 319 GTGANGTGTCCAGCCACGTCACACAGGTGACCCCTGGCCCTGACAGAGACCTTCCCG 378
 Db 130 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlnTrpPhePro 149
 QY 379 CCGGGATGCGCTGGCTGGCTACTGGCTGGGCGGATGTCGAGACAAATGATGAGGGCCCTCCA 438
 Db 150 ProGIyMePrOCySTrYrValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 169
 QY 439 CCGCCATTTCCTGTGAGCAGGTGAAGGTCGCCATTAATGGAACCAACCATTTGTGACGCA 498
 Db 170 ProPrOPhePrOleuLysGlnValLysValProIleMeGluAsnHisIleCysAspAla 189
 QY 499 AAATACACACCTTGGCCCTTACACGGGAGAGACGTCGCCATCGCTCCGTGACGACATGCTG 558
 Db 190 LysTyrHisLeuGlyAlaLeuTyrThrGlyAspAspValArgIleValIArgAspAspMetLeu 209
 QY 559 TGTGGCGGGAACACCCGGAGGACATCATGCGACGGGCGACTCCGGAGGGCCCTGGTGTGC 618
 Db 210 CysAlaGlyAsnTrpThrArgTrpAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 229
 QY 619 AAGGTGAATGGACACCTGGCTGAGGGGGCGTGCAGCTGGGGGGGAGGGGCGTGGCCGAC 678
 Db 230 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 249
 QY 679 CCCAACGGGCTGGGATCTTACACCCGCTGTACACCTACTACTGACTGACTGATCCACCACTAT 738
 Db 250 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 269
 QY 739 GTCCCAAAAACCCG 753
 Db 270 ValProLysLysPro 274

RESULT 4

US-08-978-404B-16
 ; Sequence 16, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TIME OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston

US-09-598-982-20 (1-771) x US-09-016-366A-19 (1-273)

19 ATGCGGGGGTTCAGAGGGGGCCCGAGGAGCAAGTGGCCCTGGAGGCTGAGAGTGC 78
29 ILeValGIGlyGlnGlnAlaIarProIarGserIystrPrroIarGlnValSerLeuIarGlyAl 48
79 CAGCGCCCATCTAGATGATGACATCTTGGCGGGGGCTCCCTCATGCAACCCCACTGGGTGCTG 138
49 HisGlyProIytrTmehNisRhecysGlyIySerLeuIleHisProGlnItrrValIleu 68
139 ACCGCGCGGGCTGGCTGGGAGACCCGAGGCTCAAGATCTGGCCCGCTGAGGGTGCACATG 198
69 ThrIAlaIaniScySvalGlyrProAspValIlySAspLeuAlaIalaIeudrGValGlnIleu 88
199 CGGGAGCAGCACTCTACTACCAGGAGCCAGTGGTGGCGGTCAGAGGATGATGCTGGCAC 258
89 ArgGlnGlnHisLeuIytrTyrGlnAspGlnIleuLeuProValSerArgIleIleValHis 108
259 CCACAGTTCATACACCCGAGATGCGAGGAGACATCCGCTGCTGGAGCTGAGAGGCGG 318
109 ProGlnPheIytrThrAlaGlnIleGlyAlaAspIleAlaIeuleuGlnIleuGlnIuPro 128
319 GTGAAGGTCTCCAGCCACAGCTCCACAGGCTCACCCCTGGCCCTGAGAGACTTCCCC 378
129 ValAsnValIserSerHisValHisThrValIthrLeuProProIaIaSerGIuThrPhePro 148
379 CGGGGATGGCGTGGTGGTTCATCTGGTGGGGGATGGAGATGATGATGAGAGCTGCCCA 438
149 ProGlyMetProCysItrrValIthrGlyItrrPglIyAspValaIAspAsnAspGlnIarGlyeuro 168
439 CCGCCATTTCCCTGAGAGCAGGTGAAGGTCCCAATGATGAAACACCATTTTGTGACGCA 498
169 ProIarPheProIeuleuIyGlnValIlySValIProIleMetGluAsnHisIleCysAspAla 188
499 AAATPACCACTTGGCGCTTACAGCGGAGAGAGAGAGCTCCGATCTGCCCTGACAGACATGCTG 558
189 LysTyrHisIleuGlnIyAlaIytrThrGlyIyAspAspValaIArgIleValaIArgAspAspMetLeu 208
559 TGTGCGGGGAGACACCCGAGGAGACTCATGCCAGGCGGACCTCCGAGGCGCCCTGGTGTGC 618
209 CysAlaGlyAsnItrrArgArgAspSerCysGlnGlyAspSerGlyGlyProIeuleuValCys 228
619 AAGGTGAATGCGACCTGGCTGACAGCGGGGCTGGTCACTGGCGGAGGGCTGTGGCCAG 678
229 LysValAsnGlyItrrItrrPleuGlnIalagIyAlaIyAlaIserItrrPglIyGlyCysAlaGln 248
679 CCGAAGCGGCTGGCATCTACACCCGCTGTCACCTAATGATGAAACACCATTTTGTGACGCA 738
249 ProAsnArgProGlyIleIytrThrArgValIthrIytrIyLeuAspItrrIleHisHisIytr 268
739 GTCCGCAAAAANGCGG 753
269 ValProIyLysPro 273

RESULT 6
US-08-978-404B-14
Sequence 14, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
US-08-978-404B-14

Alignment Scores:
Prod. No.: 1.33e-102
Score: 1363.00
Percent Similarity: 99.18%
Best Local Similarity: 99.18%
Query Match: 2
Gaps: 0
US-09-598-982-20 (1-771) x US-08-978-404B-14 (1-273)
19 ATGCGGGGGTTCAGAGGGGGCCCGAGGAGCAAGTGGCCCTGGAGGCTGAGAGTGC 78
29 ILeValGIGlyGlnGlnAlaIarProIarGserIystrPrroIarGlnValSerLeuIarGlyAl 48
79 CAGCGCCCATCTAGATGATGACATCTTGGCGGGGGCTCCCTCATGCAACCCCACTGGGTGCTG 138
49 HisGlyProIytrTmehNisRhecysGlyIySerLeuIleHisProGlnItrrValIleu 68
139 ACCGCGCGGGCTGGCTGGGAGACCCGAGGCTCAAGATCTGGCCCGCTGAGGGTGCACATG 198
69 ThrIAlaIaniScySvalGlyrProAspValIlySAspLeuAlaIalaIeudrGValGlnIleu 88
199 CGGGAGCAGCACTCTACTACCAGGAGCCAGTGGTGGCGGTCAGAGGATGATGCTGGTGCAC 258
89 ArgGlnGlnHisLeuIytrTyrGlnAspGlnIleuLeuProValSerArgIleIleValHis 108
259 CCACAGTTCATACACCCGAGATGCGAGGAGACATCCGCTGCTGGAGCTGAGAGGCGG 318
109 ProGlnPheIytrThrAlaGlnIleGlyAlaAspIleAlaIeuleuGlnIleuGlnIuPro 128
319 GTGAAGGTCTCCAGCCACAGCTCCACAGGCTCACCCCTGGCCCTGAGAGACTTCCCC 378
129 ValAsnValIserSerHisValHisThrValIthrLeuProProIaIaSerGIuThrPhePro 148
379 CGGGGATGGCGTGGTGGTTCATCTGGTGGGGGATGGAGATGATGATGAGAGCTGCCCA 438
149 ProGlyMetProCysItrrValIthrGlyItrrPglIyAspValaIAspAsnAspGlnIarGlyeuro 168
439 CCGCCATTTCCCTGAGAGCAGGTGAAGGTCCCAATGATGAAACACCATTTTGTGACGCA 498
169 ProIarPheProIeuleuIyGlnValIlySValIProIleMetGluAsnHisIleCysAspAla 188
499 AAATPACCACTTGGCGCTTACAGCGGAGAGAGAGAGCTCCGATCTGCCCTGACAGACATGCTG 558
189 LysTyrHisIleuGlnIyAlaIytrThrGlyIyAspAspValaIArgIleValaIArgAspAspMetLeu 208

QY 559 TGTCGGGGAACACCCGGAGGACTCAGCCAGGCGGACCTCCGGAGGGCCCTGGTGTGC 618
 |||||||
 Db 209 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 228
 QY 619 AAGGTGAATGGACACCTGGCTGGCAGAGCGGGCTGTCACTGAGCTGGGGCCGAGGGCTGTGCCAG 678
 |||||||
 Db 229 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyGlyCysAlaGln 248
 QY 679 CCCAAAGGGCTGGCATCTACACCCGGTGCACCTACTGACTGGACCTGGATCCACCACTAT 738
 |||||||
 Db 249 ProAsnArgProGlyIleTrpIleArgValThrTrpTrpLeuAspTrpIleHisHisTyr 268
 QY 739 GTCCCAAAAAAGCCG 753
 |||||||
 Db 269 ValProLysLysPro 273

RESULT 7

US-09-016-366A-23
 ; Sequence 23, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELETYPE:
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-016-366A-23

Alignment Scores:
 Pred. No.: 4,54e-101 Length: 267
 Score: 1344.00 Matches: 241
 Percent Similarity: 98.37% Conservative: 4
 Best Local Similarity: 98.37% Mismatches: 4
 Query Match: 92.18% Indels: 0
 Gaps: 2

US-09-598-982-20 (1-771) x US-09-016-366A-23 (1-267)
 QY 19 ATCGTCGGGGGTCAAGAGGCCCGGCAAGTGGCCCTGGCAGGTGAGCCCTGAGAGTGC 78
 |||||||

Db 23 IleValGlyGlyInGluAlaIleProArgSerLysTrpProTrpGlnValSerLeuArgVal 42
 QY 79 CAGCGCCCATACATGATGATGACTTCTGGGGGGCTCCCTCATCCAGCCCGAGGGTGTCTG 138
 |||||||
 Db 43 ArgAspArgTrpTrpMetHisPheCysGlyLysSerLeuIleHisProGlnTrpValLeu 62
 QY 139 ACCCGCCGGGGCTGGAGCCGAGCCGATCAAGGATCCGGCCCGCCCTCAGGATCCAACTG 198
 |||||||
 Db 63 ThrIleAlaHisCysValGlyProAspValLysAspLeuIleAlaLeuArgValGlnLeu 82
 QY 199 CGGAGCAGCACCTCTACTACACAGGACAGCAGCTGTCCGCTCAGCAGGATCATGTGCAC 258
 |||||||
 Db 83 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 102
 QY 259 CCACAGTTTCTACACCGCCAGATGCGGGAGGAGATGCGCCCTGGCTGGAGCTGGAGGACCG 318
 |||||||
 Db 103 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuGlnPro 122
 QY 319 GTGAAGGTCTCCACACGATCCACAGCAGCTCCAGCCCTGGCCCTCAGAGACCTTCCCC 378
 |||||||
 Db 123 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlnThrPhePro 142
 QY 379 CCGGGATGCCGCTGTGGTACTGCTGGGGCGATGTGACAAATGATGAGCCCTTCCCA 438
 |||||||
 Db 143 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGlnArgLeuPro 162
 QY 439 CCGCATTTCTCTGAGAGCAGGTGAGGTCGCCCAATATGGAACAACCATTTGTGACGCA 498
 |||||||
 Db 163 ProProPheProLeuLysGlnValLysValProIleMetGlnHisIleCysAspAla 182
 QY 499 AAATATCCACTTTGGCCCTTACACAGGAGAGCAGCTCCGATCGTCCGTGACAGCATCTCTG 558
 |||||||
 Db 183 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValAlaGlyAspAspMetLeu 202
 QY 559 TGTCGGGGAACACCCGGAGGACTCATGCCAGGGCCACTCCGAGGGCCCTGGTGTGC 618
 |||||||
 Db 203 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 222
 QY 619 AAGGTGAATGGACACCTGGCTGGCAGAGCGGGCTGTCACTGAGCTGGGGCCGAGGGCTGTGCCAG 678
 |||||||
 Db 223 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyGlyCysAlaGln 242
 QY 679 CCCAAAGGGCTGGCATCTACACCCGGTGCACCTACTGACTGGACCTGGATCCACCACTAT 738
 |||||||
 Db 243 ProAsnArgProGlyIleTrpIleArgValThrTrpTrpLeuAspTrpIleHisHisTyr 262
 QY 739 GTCCCAAAAAAGCCG 753
 |||||||
 Db 263 ValProLysLysPro 267

RESULT 8

US-08-978-404B-18
 ; Sequence 18, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B

QY 19 ATCGTGGGGGTACAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCCTGAGAGTTC
 |||
 1 TLevalGlyGlnGlnAlaProArgSerLysTrpProTArgLInValSerLeuArgVal 20
 QY 79 CACGGCCCACTACTGGATGACATTTCGGGGGGGCTCCCTATCCACCCTGAGTGGGTGTC 138
 |||
 21 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnInTrpValLeu 40
 QY 139 ACCGGCCGGGGGTGGGAGCCGGGACGTCAGAGGATCTGGCCGCTTCAGGGGGCAACTG 198
 |||
 41 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeu 60
 QY 199 CCGGAGCAGCAGCAGCAGTACTACAGAGGAGCAGCAGCAGTCCCGGCTCCGAGCAGGATCTGTCAC 258
 |||
 61 ArgGlnGlnHisLeuTyrLysGlnAspGlnLeuLeuProValSerArgLysIleValHis 80
 QY 259 CCACAGTGTACACCCCGACATCGAGCGGACATCGCCCTGGTGGAGCGTGGAGAGCGG 318
 |||
 81 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnIleGlnGluPro 100
 QY 319 GTGAAGGTCTCCAGCCAGTCCACAGCAGGTCACCCCTGGCCCTCAGAGACCTTCGCC 378
 |||
 101 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerLInTrpPhePro 120
 QY 379 CCGGGGATCCGCTGGTGGTCACTGGCTGGGCGAGATGTGGACAAATGATGAGCCCTCCCA 438
 |||
 121 ProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAspGluProLeuPro 140
 QY 439 CCGCCATTTCTCTGACAGCAGGTGAAGTCCCGCATATGGAAGAACCCACATTTGTGACGCA 498
 |||
 141 PropProPheProLeuLysGlnValLysValProIleMetGlnValHisIleCysAspAla 160
 QY 499 AATATCACCTTGGGGGCTACACAGGAGAGCAGAGTCCGGCATCGTCCGTGACGACATGCTG 558
 |||
 161 LysTyrHisLeuGlyAlaIleTyrThrGlyAspAspValArgIleLeuArgAspSerMetLeu 180
 QY 559 TGTGGCCGGAACACCCCGGAGGATCTCCAGAGGCGAGCTCCGAGGCGCCCTGGTGTGTC 618
 |||
 181 CysAlaGlyLysSerGlnArgAspSerCysLysGlyAspSerGlyLysProLeuValLys 200
 QY 619 AAGGTGATMGACACTGGCTGCAGCGGGCGGCTGGTGGTGGAGCGGCGTGTGCCGCA 678
 |||
 201 LysValAsnGlyThrTrpLeuGlnAlaGlyValIleSerTrpAspGluCysAlaGln 220
 QY 679 CCCAACCCGGCCGGATCTACACCCGCTGCACCTACTCTGATGGATGACCACTATP 738
 |||
 221 ProAsnArgProGlyIleTyrThrArgValInTrpTyrLeuAspTrpIleHisHisTyr 240
 QY 739 GTCCCCAAAAAGCCG 753
 |||
 Db 241 ValProLysLysPro 245
 DB
 RESULT 10
 US-09-016-366A-17
 ; Sequence 17, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chiu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; NUMBER OF SEQUENCES: 65
 ; CORESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEFX:
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-016-366A-17
 Alignment Scores:
 Pred. No.: 2.07e-95 Length: 275
 Score: 1274.00 Matches: 226
 Percent Similarity: 94.69% ConservatIve: 6
 Best Local Similarity: 92.24% Mismatches: 13
 Query Match: 87.38% Indels: 0
 DB: 2 Gaps: 0
 US-09-598-982-20 (1-771) x US-09-016-366A-17 (1-275)
 QY 19 ATCGTGGGGGTACAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCCTGAGAGTTC 78
 |||
 31 TLevalGlyGlnGlnAlaProArgSerLysTrpProTArgLInValSerLeuArgVal 50
 Db 79 CACGGCCCACTACTGGATGACATTTCGGGGGGGCTCCCTATCCACCCTGAGTGGGTGTC 138
 |||
 51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnInTrpValLeu 70
 QY 139 ACCGGCCGGGGGTGGGAGCCGGGACGTCAGAGGATCTGGCCGCTTCAGGGGGCAACTG 198
 |||
 71 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeu 90
 Db 199 CCGGAGCAGCAGCAGTACTACAGAGGAGCAGCAGTCCCGGCTCCGAGCAGGATCTGTCAC 258
 |||
 91 ArgGlnGlnHisLeuTyrLysGlnAspGlnLeuLeuProValSerArgLysIleValHis 110
 QY 259 CCACAGTGTACACCCCGACATCGAGCGGACATCGCCCTGGTGGAGCGTGGAGAGCGG 318
 |||
 111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGlnIleGlnGluPro 130
 Db 319 GTGAAGGTCTCCAGCCAGTCCACAGCAGGTCACCCCTGGCCCTCAGAGACCTTCGCC 378
 |||
 131 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 150
 QY 379 CCGGGGATCCGCTGGTGGTCACTGGCTGGGCGAGATGTGGACAAATGATGAGCCCTCCCA 438
 |||
 151 ProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAspGluProLeuPro 170
 Db 439 CCGCCATTTCTCTGACAGCAGGTGAAGTCCCGCATATGGAAGAACCCACATTTGTGACGCA 498
 |||
 171 PropProPheProLeuLysGlnValLysValProIleMetGlnValHisIleCysAspAla 190
 QY 499 AATATCACCTTGGGGGCTACACAGGAGAGCAGAGTCCGGCATCGTCCGTGACGACATGCTG 558
 |||
 191 LysTyrHisLeuGlyAlaIleTyrThrGlyAspAspValArgIleLeuArgAspSerMetLeu 210
 QY 559 TGTCCCGGGAACACCCCGGAGGACTCATGCCAGGCGACTCCGAGAGGCGCCCTGGTGTGTC 618

Db 211 CysAlaIaGlyAsnSerGlnAArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 230
 QY 619 AAGGTGAATGGACACCTGGCTGGAGCGGGCGTGGTACCTGGGGGAGAGGGCTGTGCCAG 678
 Db 231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGlnuGlyCysAlaGln 250
 QY 679 CCCAACCGGCTGGCATGTACACCCGGTGTACCTACTTGGACTGGATCCACCACATAT 738
 Db 251 ProAsnArgProGlyIleFtyrThrArgValThrYtyrLeuAspTrpIleHisHisTyr 270
 QY 739 GTCCCAAAAAGCCG 753
 Db 271 ValProLysLysPro 275

RESULT 11
 US-08-978-404B-12
 ; Sequence 12, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ. ID NO.: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 5968782e
 ; US-08-978-404B-12

Alignment Scores:
 Pred. No.: 1274-95 Length: 275
 Score: 1274.00 Matches: 226
 Percent Similarity: 94.69% Conservative: 6
 Best Local Similarity: 92.24% Mismatches: 13
 Query Match: 87.38% Indels: 0
 DB: 2 Gaps: 0
 US-09-598-982-20 (1-771) x US-08-978-404B-12 (1-275)
 QY 19 AATGCTGGGGGTCAGAGAGCCCAAGAGCAAGTGGCCCTGGCCAGGCTGAGCCTGAGAGTC 78
 Db 31 IlevAlGlyGlnGlnAlaIProArGserLysTrpProTrpGlnValSerLeuArGVal 50

QY 79 CACGGCCATPACTGGATGCATCTTGGGGGGCTCCCTTCACCCCAAGTGGGGTGGT 138
 Db 51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnIleTrpValLeu 70
 QY 139 ACCGCGCCGCTGGCTGGAGCCGAGCACTCAAGGATCTGGCCGCTCAGCGGTGCAACTG 198
 Db 71 ThrAlaIleHisCysIleuGlyProAspValLysAspRleAlaIleThrLeuArgValGlnLeu 90
 QY 199 CCGAGACACACCTACTACAGGACACAGCTGTCCGCGGTGAGCAGGATCATCTGTGAC 258
 Db 91 ArgGlnGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis 110
 QY 259 CCAAGTTCCTACACCCCAAGTCCGAGCGGAGCAATCCGCTCCGAGGTGGAGGAGCCG 318
 Db 111 ProGlnPheTyrIleIleIleThrGlyAlaAspIleAlaLeuLeuGlnuGlnuPro 130
 QY 319 GTGAAGTCTCCAGCCACACCTCCACAGGTCACCCCTGCCCTGTCCAGAGACTTCCCC 378
 Db 131 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGlnuThrPhePro 150
 QY 379 CCGGGATGCGCTGCTGGGTCACTGGCTGGGGCGGATGTGGACAATGATGAGCGCTCCCA 438
 Db 151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGlnuProLeuPro 170
 QY 439 CCGCAATTCCTGTGAAGGAGGAAAGTCCCAATTAATGAAACCAATTTGTGACGCA 498
 Db 171 ProProPheProLeuLysGlnValLysValProIleMetGlnuAsnHisIleCysAspAla 190
 QY 499 AATATACACCTTGGCGCTTACACGGGAGACAGCAAGTCCGCTCCGCTGGAGCAATGCTG 558
 Db 191 LysTyrHisLeuGlyAlaIleTyrThrGlyAspAspValArgIleIleArgAspAspMetLeu 210
 QY 559 TGTCCCGGGAACACCCCGGAGGACTTCATGCCAGGGCGACTCCGGAGGGCCCTGGTGTG 618
 Db 211 CysAlaIaGlyAsnSerGlnAArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 230
 QY 619 AAGGTGAATGGACACCTGGCTGGAGCGGGCGTGGTACCTGGGGGAGAGGGCTGTGCCAG 678
 Db 231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGlnuGlyCysAlaGln 250
 QY 679 CCCAACCGGCTGGCATGTACACCCGGTGTACCTACTTGGACTGGATCCACCACATAT 738
 Db 251 ProAsnArgProGlyIleFtyrThrArgValThrYtyrLeuAspTrpIleHisHisTyr 270
 QY 739 GTCCCAAAAAGCCG 753
 Db 271 ValProLysLysPro 275

RESULT 12
 US-09-016-366A-15
 ; Sequence 15, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A

FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-366A-15

Alignment Scores:
Pred. No.: 1.05e-80 Length: 276
Score: 1092.00 Matches: 192
Percent Similarity: 84.80% Conservative: 20
Best Local Similarity: 76.80% Mismatches: 36
Query Match: 74.90% Indels: 2
DB: Gaps: 1

US-09-598-982-20 (1-771) x US-09-016-366A-15 (1-276)
QY 4 CCCCSTCGAAGAAAAGA-----ATCGTCGGGGGTCAGAGAGCCSCCAGAGCAAGTGGCC 57
DB 25 ProLaasnglnArGValGlylLeValGlyGlnHsGlnAlaSerGlnSerIystrPro 44
QY 58 TGGCAGGTGAGCCCTGAGAGTCCAGCCCAATGACGTGACATTTGGGGGGCTCCCTC 117
DB 45 TrpGlnValSerLeuArGpHelysLeuAsnTyrrTrpIleHsRphescysGlyGlySerLeu 64
QY 118 ATCCACCCCACTGGGTGGTGCAGCCCGGGGGTGGCGGAGGAGGAGGAGGAGTGTG 177
DB 65 ILeHsPrOGllTrpValLeuThrAlaAlaHsCysValGlyPrOHsIleLeysSerPro 84
QY 178 GCCGCGCTTCCAGGCGTCAACTGCGGGAGCAGCAGCCTTACTACTCCAGAGCCAGCTGGTGGC 237
DB 85 GlnLeuPheArGValGlnLeuArGlnGlnTyrrLeuTyrrGlyAspIleLeuSer 104
QY 238 GTCAGCAGGATGATGTGTGACCCACAGTTCACACCCCGCAGATGGAGCCAGATCCGC 297
DB 105 LeuAsnArGllLeValValHsPrOHsTyrrTrpIleAlaGlnGlyGlyAlaAspValAla 124
QY 298 CTGCTGGAGCTGGAGGAGCGGTGAAGCTCCAGCCAGTCCACAGCCAGTCCAGCCCGCC 357
DB 125 LeuLeuGlnLeuGlnValProValAsnValSerTrHsIleHsIleProIleSerLeuPro 144
QY 358 CCTGCCTCAGAGACCTTCCCGGGGGATGCCCTGTGGGTGACTGGGGCTGGGGCGATGTG 417
DB 145 ProAlaSerGlnThrPheProProGlyTrHsSerCysTrpValTrHsGlyTrpGlyAspIle 164
QY 418 GACAAATGATGAGCCCTCCAGCCAGTTCCTGTGAAGCAGGTGAAGTCCCCCATAAAG 477
DB 165 AspAsnAspGlnProlLeuProProProTyrrProLeuLysGlnValAllyValProIleVal 184
QY 478 GAAACCAACATTTGTGAGCAAAATACCACTTTGGGGCCTTACAGGGGAGAGAGAGCTCCGC 537
DB 185 GluAsnSerLeuCysAspArgIystrTrHsTrHsGlyLeuTyrrTrHsGlyAspAspPhePro 204
QY 538 ATCGTCCTGAGCAGATGCTGTGTGGCGGGAACACCCGGAGGAGACTCATGCCAGGGCGAGC 597
DB 205 ILeValHsAspGlyMetLeuCysAlaGlyAsnTrHsArgArGAspSerCysGlnGlyAsp 224
QY 598 TCCGGAGGGCCCTGGGTGTGCAAGGTAAATGGCACCTGGCTCCAGGCGGGCGTGTCAAGC 657

DB 225 SerGlyGlyProlLeuValCysIysValIyysGlyTrHrPleuGlnAlaGlyValValSer 244
QY 658 TGGGCGAGGGCTGTGCCAGCCCAACCGCGCTGCATCTACACCCGTCGACCTACTAC 717
DB 245 TrpGlyGlnGlyCysAlaGlnProlAsnIystrProGlyIleTyrrTrHsArgValTrHsTyrr 264
QY 718 TTGACGTGAGTCCACCACTATGTCCCAAA 747
DB 265 LeuAspTrpIleHsArgIyValProGlu 274

RESULT 13
US-08-978-404B-21
Sequence 21, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacks, P. C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
US-08-978-404B-21
Alignment Scores:
Pred. No.: 1.05e-80 Length: 276
Score: 1092.00 Matches: 192
Percent Similarity: 84.80% Conservative: 20
Best Local Similarity: 76.80% Mismatches: 36
Query Match: 74.90% Indels: 2
DB: Gaps: 1
US-09-598-982-20 (1-771) x US-08-978-404B-21 (1-276)
QY 4 CCCCSTCGAAGAAAAGA-----ATCGTCGGGGGTCAGAGAGCCSCCAGAGCAAGTGGCC 57
DB 25 ProLaasnglnArGValGlylLeValGlyGlnHsGlnAlaSerGlnSerIystrPro 44
QY 58 TGGCAGGTGAGCCCTGAGAGTCCAGCCCAATGACGTGACATTTGGGGGGCTCCCTC 117
DB 45 TrpGlnValSerLeuArGpHelysLeuAsnTyrrTrpIleHsRphescysGlyGlySerLeu 64

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2003, 05:24:20 ; Search time 46 seconds
(without alignments)
4466.793 Million cell updates/sec

Title: US-09-598-982-20
Perfect score: 1458
Sequence: 1 gggccccctcagaagaagaat.....cgtgaagcggccgcctcgt 771

Scoring table: BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Fgapop 10.0 , Fgapext 0.5
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 20
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DBY=xjh
-Q/cgr2_1/USPTO_Spool/US09598982/rnat_27012003_073715_19505/app_query.fasta_1.967
-DB-A=geneseq.101002 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982.cgn.1.1.0.urnat.27012003.073715.19505 -NCPU=6 -TCPu=3
-NO_XLPRY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WANN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A.Geneseq.101002:*
1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1393	95.5	249	AAU12009	Human beta-II tryp
2	1388	95.2	249	AAU12017	Human beta-II tryp
3	1387	95.1	249	AAV55011	Human beta-tryptas
4	1387	95.1	249	AAU12007	Recombinant human
5	1384	94.9	249	AAU12011	Human beta-II tryp
6	1384	94.9	249	AAU12012	Human beta-II tryp
7	1382	94.8	249	AAU12006	Human beta-I tryp
8	1379	94.6	249	AAU12010	Human beta-II tryp
9	1379	94.6	249	AAU12019	Human beta-II tryp
10	1379	94.6	249	AAU12020	Human beta-II tryp
11	1374	94.2	245	AAU12013	Human beta-II tryp
12	1374	94.2	245	AAU12018	Human beta-II tryp
13	1369	93.9	245	AAU12021	Human beta-II tryp
14	1368	93.8	245	AAU12008	Recombinant human
15	1368	93.8	274	AAW64240	Human mast cell tr
16	1368	93.8	274	AAW63175	Human mast cell tr
17	1365	93.6	245	AAU12015	Human beta-II tryp
18	1365	93.6	245	AAU12016	Human beta-II tryp
19	1363	93.5	245	AAV55010	Human beta-tryptas
20	1363	93.5	245	AAU12005	Human mature beta-
21	1363	93.5	273	AAW64238	Human mast cell tr
22	1363	93.5	273	AAW63174	Human mast cell tr
23	1361	93.3	244	AAV25925	Human lung mast ce
24	1360	93.3	245	AAU12014	Human beta-II tryp
25	1360	93.3	245	AAU12023	Human beta-II tryp
26	1360	93.3	245	AAU12024	Human beta-II tryp
27	1355	92.9	245	AAU12022	Human beta-II tryp
28	1344	92.2	267	AAW64241	Human mast cell tr
29	1344	92.2	267	AAW63176	Human mast cell tr
30	1344	92.2	267	AAU84360	Protein TP52 diffe
31	1329	91.2	691	AAE14348	Human protease PRP
32	1274	87.4	275	AAW64237	Human mast cell tr
33	1274	87.4	275	AAW63173	Human mast cell tr
34	1092	74.9	276	AAW64242	Murine mast cell p
35	1092	74.9	276	AAW63172	Mouse mast cell pr
36	1077	73.9	276	ABB05437	Mouse mast cell pr
37	1075	73.7	270	AAW64239	Gerbil homologue o
38	1057	72.5	273	AAW64233	Murine MCP-7 zymo
39	1057	72.5	310	AAE14343	Human protease PRP
40	1055	72.4	274	AAW64234	Rat homologue of m
41	1039	71.3	273	AAW64235	Rat homologue of m
42	1006	69.0	273	AAV81826	Pig lung protease.
43	702	48.1	190	AAW68539	Amino acid sequenc
44	698	47.9	190	AAW68540	Amino acid sequenc
45	684.5	46.9	269	AAW64236	Canine homologue o

ALIGNMENTS

RESULT 1
AAU12009 standard; Protein: 249 AA.
AAU12009; 09-APR-2002 (first entry)

Human beta-II tryptase active site mutant H44A #1.
Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
enzyme; mutant; mutlein.
Homo sapiens.
Synthetic.
MO200198470-A2.
27-DEC-2001.

XX 20-JUN-2001; 2001MO-US19681.
 PF
 XX 21-JUN-2000; 2000US-0598982.
 PR
 XX (PROM-) PROMEGA CORP.
 PA
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX
 DR WPI: 2002-114578/15.
 DR N-PSDB; AAS20775.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PT an active site mutation -
 XX
 PS Claim 8; Page 84-85; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modeling studies. The
 CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II tryptase active site mutants.
 CC
 CC Sequence 249 AA:
 XX
 XX

Alignment Scores:
 Pred. No.: 1 43e-97 Length: 249
 Score: 1393.00 Matches: 249
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.54% Indels: 0
 DB: 23 Gaps: 0

US-09-598-982-20 (1-771) x AAU12009 (1-249)

QY 7 CTCGAGAAAAGATCTGCGGGGTCAAGGAGCCSCCAAGSAAAGTGGCCCTGGCAGGTG 66
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 LeuGIuYsAtgIleValIGlyGIgInGluAlaProAtgSerLysTrpProTfRgInVal 20
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 67 AGCCTGAGAGTCCACGGCCCACTACTGGATGCACTTTCGGGGGCTCCCTATGCCACCC 126
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 21 SerLeuAlrValInHISglYrProTyrTrpMetHISphecYsGIYglYSerLeuIIHISPro 40
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 127 CAGNGGGGTCAGCCGGCCGGGGGGTGGGAGCCGAGCCGTCAGAGATCTGGCCGCTC 186
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 41 GIInTrPAlleuPrOAlaValAlaAlaIaCysValAlDyProAspValLysAspLeuAlaHLeu 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 187 AGGCTGCAACTGGCGGAGCAGCACCTTACTTACAGAGACAGCACTGCTCCGGTCAAGCAGG 246
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ArgValAlGInLeuAlrGluGIuGInHISleuYrTyrGInAspRGIuLeuPrOValSerArg 80
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 247 ATCATCGTGCACCCACAACTGTCTAACACCGCCCAAGATGGAGCGGACATGCGCTGGAG 306
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 81 IleIleValInHISpRogInPrHethrYrThrAlaGInIleGlyAlaAspIleAlaLeuLeuIu 100
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 307 CTGAGAGCGCGGGAAGGTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 366
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 101 LeuGIuYsAlrProAlLysValSerSerHISValIHISrInrValIThrLeuPrOProAlaSer 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 367 GAGACCTTCCCGCGGGATGCGGTGCTGACTGCGTGGGGGATGTGGACAAATGAT 426
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 GIInTrPAlleuPrOAlaValAlaAlaIaCysValAlDyProAspValLysAspLeuAlaHLeu 140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 427 GAGCGCTCCACCCGATTTTCTGAGACAGGTGAAGGTCACCAATATGAAACACAC 486
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 141 GIuArGIeUPrOPrOPrOleuLysGIuValLysValIProIIeMetGIuAsnHIS 160
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 487 ATTTGTGACCCAAATATACCACTTGGCCCTTACACGGAGACAGCACTCCCATCTGTCCT 546
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 161 IleCysAspAlaLysrYrHISleuGIuAlaTyrThrGIuYsAspAspValAlrGlyIleValAlrG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 547 GAGCACAATGCTGTGTGGCCGAGACACCCGGAGAGACATGATCCAGGGCCACTCGGAGGG 606
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AspAspMetLeuCysAlaGIYsHnThrAlrGAspSerCysGIuGIYAspSerGIYGIY 200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 607 CCCCTGGGTCAGAGGTGAATGATGGCACCCTGGCTGACGGCCGCTGTCAGCTGGGGCGAG 666
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 201 PrOleuValCysLysValAsnGIYThrTrPleuGIuAlaGIYValISeITrPGLYGIu 220
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 667 GGCTGTGCGCCCAAGCCAGCCGCTGGCATCTACACCCGCTGTCACCTACTTGGACTGG 726
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 221 GIYcysAlaGInPrOAsnArGPrOGIYIleTyrThrArGValIThrYrYrLeuAspTrp 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 727 ATCCACCACTATGTCCCAAAAAGCCG 753
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 IleHISrYrValIProLYsLysPro 249
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2
 AAU12017
 ID AAU12017 standard; Protein: 249 AA.
 XX
 AC AAU12017;
 XX
 DF 09-Apr-2002 (first entry)
 XX
 DE Human beta-II tryptase active site mutant H44A #3.
 XX
 KW Human: proteolytic tryptase; protease; recombinant beta-II tryptase;
 KM enzyme; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001MO-US19681.
 PF
 XX 21-JUN-2000; 2000US-0598982.
 PR
 XX (PROM-) PROMEGA CORP.
 PA
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX
 XX WPI: 2002-114578/15.
 DR N-PSDB; AAS20783.
 DR
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PT an active site mutation -
 XX
 PS Claim 8; Page 105-106; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active

CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II tryptase active site mutants.
 CC
 XX
 XX
 SQ Sequence 249 AA:

US-09-598-982-20 (1-771) x AAU12017 (1-249)

Alignment Scores:	3.41e-97	Length:	249
Pred. No.:	1388.00	Matches:	248
Score:	99.60%	Conservative:	0
Percent Similarity:	99.60%	Mismatches:	1
Best Local Similarity:	95.20%	Indels:	0
Query Match:	23	Gaps:	0
DB:			
OY	7	CTCGAGAAAAGAAATCGTGGGGTTCAGAGAGCCGCCAGGACAAATGCGCCCTGGCAGGTG	66
Db	1	LEGLULYSARGILEVALGILYGLINGLUALAPROARGSERLYSTRPSTRPSTRPGLVAL	20
OY	67	AGCCCTGAGAGTCCAGCCGCCATTAATCTGATGATGACCTTCTGGGGGGTCCCTCATCCACCC	126
Db	21	SERLEAARVALHISGLYPRORYTRTPMETHISPHCYSGILYLSERLEULIENHISPRO	40
OY	127	CAGTGGGTCTGACCCGCCGGCGTGGGACCCGGACCGTCAAGGATCTGGCCGCCCTC	186
Db	41	GINTXPVALLEUTHRLAALAAIACYSVALGILYPROASPVALLYSAPREUHALAALAEU	60
OY	187	AGGTGCAACTGCGGGAGACGACCTTACTACAGACCGACCGTGTGCGCGGTGACAGG	246
Db	61	ARGVALGLNLEADRGINDLNHISLEUYTYRGLNAPSLNLEUPEUROVALSERARG	80
OY	247	ATCATGCTGACCCAGATGTTTACACCGCCAGATGGAGCGGACATCGCCCTGGTGGAG	306
Db	81	IEILEVALHISPROGLNHERYTRHRLAAGLNILEGLYALAAAPLLEALALEUAEUGLU	100
OY	307	CTGGAGAGCCGGTGAAGTCTTCCAGCCAGCTCCACACCGTCCACCCCTGCCCTCA	366
Db	101	LEGLULGILPVALSVALSERSERHISVALHISITRVALIHLRLEUPROPRALASER	120
OY	367	GAGACCTTCCCGGGGATGCCGCTGGTGTCTGCTGGTGGGCGATGTGGACATGAT	426
Db	121	GLUTHPHERPROGLYMETPROCYSTRPVALLTRGILYTRPELYASPVALASPASNASP	140
OY	427	GAGCGCTCCCAACCCATTTCTTGAAGCAGAGGTGAGGTTCCCATATMGAAAACAC	486
Db	141	GLUARGLEUPROPROPHEROLEUYSGLNVALLYSVALPROILEMETGLUASNHIS	160
OY	487	ATTTGTGAGCAAAATACACCTTGGGCGCTACACGGGAGACGACGCTCCGCATGTC	546
Db	161	IECYSASPAIDLYSTRHISLEUGIYALATYRTRGILYASPSAPVALARGLILEVAL	180
OY	547	GAGGAGACTGCTGCTGGGAAACACCGGAGGAGACTCATMCCAGGGCCACTCCGAGGG	606
Db	181	ASPSAPMELIENCYSALADLYASNTRHARGARGASPSERCSGLNGLYASPSERGLYGLY	200
OY	607	CCCTGTGTGGCAAGGTGAATGGACCTGGCTGCAGGGCGGCTGGTCAAGCTGGGCGAG	666
Db	201	PROLEUVALCYSTYSVALNSNGLYTRHTRPLEUENGLNALSGLYVALSERTRPGLYGLU	220
OY	667	GGCTGTGCCAGCCCAACCGCCCTGGCATCTACACCCGTGTCACCTACTATGAGCTGG	726
Db	221	GLYCYALAGILNPROASNARTRPGLIETERYTRHARGVALIHLRTRTYRLEUAEPTRP	240
OY	727	ATPCACCACTATGTCGCCCAAAAAGCGG	753
Db	241	IENHSHISTYTRVALPROLYSYPRO	249

RESULF 3
 AA55011
 ID AA55011 standard; Protein; 249 AA.
 AC AA55011;
 AC AA55011;
 DT 18-FEB-2000 (first entry)
 XX
 XX
 DE Human beta-tryptase protein sequence.
 KW Beta-tryptase; human; DNA expression construct; protein production;
 KW combinatorial library screening; X ray crystallography; antigen;
 KW antibody generation.
 OS Homo sapiens.
 PN W09960139-A1.
 PD 25-NOV-1999.
 PF 29-OCT-1998; 98WO-US22994.
 PR 15-MAY-1998; 98US-0079970.
 PA (PROM-) PROMEGA CORP.
 PI Maffitt MA.; Niles AL; Haak-Frendscho M;
 DR WPI: 2000-053300/04.
 DR N-PSDB; AA240175.
 PT New DNA expression construct for production of enzymatically active
 PT recombinant human beta-tryptase
 PS
 PS Disclosure; Page 43-44; 50pp; English.
 CC
 CC This sequence is the human beta-tryptase. The invention relates to a
 CC DNA expression construct comprising (5' to 3') a promoter linked to a
 CC signal sequence which is linked to a sequence encoding human
 CC beta-tryptase. The DNA construct is useful for transforming host cells to
 CC express, post translationally process and secrete enzymatically active
 CC human tryptase. The method is useful for the production of large amounts
 CC of tryptase with defined specificities. The transformant is useful for
 CC pharmacological studies, combinatorial library screens and X ray
 CC crystallographic studies. The tryptase produced allows for the
 CC development of tryptase agonists and/or antagonists, is useful as an
 CC antigen to generate antihuman tryptase antibodies in various animals,
 CC can be used in screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists etc. and to assay for the presence of tryptase in
 CC biological or other solutions. Tryptase inhibitors, antagonists, agonists
 CC etc. may be useful as therapeutics. The tryptase does not require any
 CC post-expression or post-purification modifications or manipulations to
 CC initiate tryptase activity and it has enzymatic activity which compares
 CC favourably with cadaveric tryptase. The availability of enzymatically
 CC active tryptase facilitates the large scale screening of combinatorial
 CC libraries for specific tryptase inhibitors as potential therapeutical
 CC advances the understanding of the biological significance of tryptase in
 CC mast cell mediated diseases. The tryptase can be used to detect low
 CC levels of tryptase.
 CC
 XX
 XX
 SQ Sequence 249 AA:

Alignment Scores:	4.06e-97	Length:	249
Pred. No.:	1387.00	Matches:	248
Score:	99.60%	Conservative:	0
Percent Similarity:	99.60%	Mismatches:	1
Best Local Similarity:	95.13%	Indels:	0
Query Match:	21	Gaps:	0
DB:			
OY	7	CTCGAGAAAAGAAATCGTGGGGTTCAGAGAGCCGCCAGGACAAATGCGCCCTGGCAGGTG	66

```

Db      1 LeuGIuLysArgIleValGIyGInGInLualAProArGSerLysrPrroTrpGlnVal 20
QY      67 AGCCTGAGAGTCCAGGGCCCATACATGATGACATCTGTGGGGGGTCCCTCATCCACCC 126
Db      21 SerLeuArgValNHISGLYrPrroTrpMetNHISphecysGlyGlySerLeuLeuHISPro 40
QY      127 CAGTGGGTGCTGACCCCGCCGGCGTGGCGGGAGCCGGATCAAGGATCTGGCCCGCTC 186
Db      41 GlnTrpValLeuThrAlaAlaHisCysValGIYProArSValLlysAspLeuAlaLeu 60
QY      187 AGGGTGCACATCCGGGAGCAGCACCCCTACTACACAGGACCAACCTGGCTGGCTGACAG 246
Db      61 ArgValGlnLeuArgGlnGlnHISLeuYrTYrGlnAspGlnLeuLeuProValSerArg 80
QY      247 ATCATCGTGCACCCACAGTCTACACCCCGCCAGATCGGAGCGGACATGCCCTGGTGGAG 306
Db      81 IleIleValNHISrProGlnPheTYrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGln 100
QY      307 CTGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACCGGTCAACCCCTGGCCCTCA 366
Db      101 LeuGIuGlnrProValLysValSerSerNHISValHISThrValThrLeuProProAlaSer 120
QY      367 GAGACCTTCCCGCCGGGAGTGGCGGTGGTCACTGGCTGGGGCGCATGGACAAATGAT 426
Db      121 GlnTrpPheProProGIYMetProCysrPrValThrGIYrPrGIYAspValAspAsnAsp 140
QY      427 GAGCGCTCCCGCCAGTTCCTGTGAAAGCGTGAAGCGTGAAGCGTCCCATATGGAAAAACAC 486
Db      141 GlnAlaGlnrProProPheProLeuLysGlnValLysValProIleMetGlnAsnHIS 160
QY      487 AATTGTGACGCAAAATATCCACCCTTGGCCCTACAGCGGAGACAGCTCCGCATTCCTCG 546
Db      161 IleCysAspAlaLysrYrHisLeuGIYAlaYrThrGlnYrAspAspAlaArgIleValArg 180
QY      547 GACGACATGCTGTGTCCGGGAGACACCCGGGAGGACTATGCCAAGGGCGATCCGGAGGG 606
Db      181 AspAspMetLeuCysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGIYGLY 200
QY      607 CCCCTGGTGGCAGAGGTAATGGACACCTGGCTGCAAGGGCGGGTGGCTGAGCGGGGCGAG 666
Db      201 ProLeuValCysLysValAsnGlnYrThrPheGlnAlaGlyValValSerTrpGIYGLY 220
QY      667 GGCCTGTGCCACCCAAACCCGGCTGGCATCTACACCCCTGTGTCACCTACTACTTGGACTGG 726
Db      221 GTCysAlaGlnrProAsnArgProGIYIeYrTrpArgValThrTYrLeuAspTrp 240
QY      727 ATCCACCACTATGTCGCCCAAAAAGCCG 753
Db      241 IeNHISHisTYrValrProLysLysPro 249
RESULT 4
AAU12007
ID      AAU12007 standard; Protein; 249 AA.
AC      AAU12007;
XX      AAU12007;
DT      09-APR-2002 (first entry)
XX      Recombinant human beta-II tryptase.
DE      Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW      enzyme; muten; mutant.
KV      Homo sapiens.
XX      Synthetic.
OS      MOZ00198470-A2.
XX      27-DEC-2001.
XX      20-JUN-2001; 2001WO-US19681.
XX

```

```

PR      21-JUN-2000; 2000US-0598982.
XX
XX      (PROM-) PROMEGA CORP.
PA
XX      Maffit M, Niles AL, Haak-Frendscho M;
PI      WPI; 2002-114578/15.
XX      N-PSDB: AAS20765.
DR
XX
XX      DNA construct for producing enzymatically-inactive proteolytic
PT      tryptase, comprises DNA sequence encoding proteolytic tryptase having
PS      an active site mutation -
XX      Claim 60; Page 77-78; 126pp; English.
XX
CC      The present invention relates to recombinant human proteolytic
CC      tryptases, active site mutants of these tryptases and the methods for
CC      producing these. The method involves the production of a DNA expression
CC      construct comprising a promoter operably linked to a secretion signal
CC      sequence which is operably linked to a DNA sequence encoding a
CC      proteolytic tryptase with an active site mutation (the construct drives
CC      expression of a mature proteolytic tryptase that lacks enzymatic activity
CC      due to the active site mutation, in hosts transformed to contain the
CC      construct). The method is useful for producing enzymatically-inactive
CC      beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC      a tool to investigate the structural and functional properties of the
CC      protease and its enzymatic activity, and for modelling studies. The
CC      enzymatically-active, recombinant proteolytic tryptase produced are
CC      useful in an antigen to generate anti-human tryptase antibodies
CC      and in drug screening for compounds which act as tryptase inhibitors,
CC      antagonists, agonists, etc. The present sequence represents recombinant
CC      human beta-II tryptase.
SQ      Sequence 249 AA:
Alignment Scores:
Pred. No.: 4.06e-97 Length: 249
Score: 1387.00 Matches: 248
Percent Similarity: 99.60% Conservat: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 95.13% Indels: 0
DB: Gaps: 0
US-09-598-982-20 (1-771) x AAU12007 (1-249)
QY      7 CTGAGAAAAGATGTCGGGGTCAAGGAGCCCGGAGGAGTGGCCCTGGCAGTNG 66
Db      1 LeuGIuLysArgIleValGIyGInGInLualAProArGSerLysrPrroTrpGlnVal 20
QY      67 AGCCTGAGAGTCCAGGGCCCATACATGATGACATCTGTGGGGGGTCCCTCATCCACCC 126
Db      21 SerLeuArgValNHISGLYrPrroTrpMetNHISphecysGlyGlySerLeuLeuHISPro 40
QY      127 CAGTGGGTGCTGACCCCGCCGGCGTGGCGGGAGCCGGATCAAGGATCTGGCCCGCTC 186
Db      41 GlnTrpValLeuThrAlaAlaHisCysValGIYProArSValLlysAspLeuAlaLeu 60
QY      187 AGGGTGCACATCCGGGAGCAGCACCCCTACTACACAGGACCAACCTGGCTGGCTGACAG 246
Db      61 ArgValGlnLeuArgGlnGlnHISLeuYrTYrGlnAspGlnLeuLeuProValSerArg 80
QY      247 ATCATCGTGCACCCACAGTCTACACCCCGCCAGATCGGAGCGGACATGCCCTGGTGGAG 306
Db      81 IleIleValNHISrProGlnPheTYrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGln 100
QY      307 CTGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACCGGTCAACCCCTGGCCCTCA 366
Db      101 LeuGIuGlnrProValLysValSerSerNHISValHISThrValThrLeuProProAlaSer 120
QY      367 GAGACCTTCCCGCCGGGAGTGGCGGTGGTCACTGGCTGGGGCGATGGACAAATGAT 426
Db      121 GlnTrpPheProProGIYMetProCysrPrValThrGIYrPrGIYAspValAspAsnAsp 140

```

QY 427 GAGCGCCGCCACCGGCATTTCTCTGTAAGCAGGTGAAGTCCCATTAATGAAAACAC 486
 |||||||
 DB 141 GIUATrgLeuPrProPhroheProleuLysGlnValIyValProIleMetGIuansHis 160
 QY 487 ATTTGTGACGCAAAATFACCACTTGGCCCTTACAGGGGAGACAGCGATCGTCCGT 546
 |||||||
 DB 161 IIECySAspAlaIlystrHisLeuGlyAlaIyTrHrGlyAspAspValArGIlleValAag 180
 QY 547 GAGCAGATGCTGTGTGCCGGAACACCCCGAGGAGACTCATGCCAGGGGACATCCGAGGG 606
 |||||||
 DB 181 AspAspMetLeuCyAlaIyAsnHrArGArGAspSerCyGlnIyAspSerGIyGly 200
 QY 607 CCCCTGTGTGCAAGGTGAATGGCACCTGGCTGCAGAGCGGGCGGTGGCTGAGTGGCCGAG 666
 |||||||
 DB 201 ProLeuValIyLysValAsnGlyTrHrTrpLeuGlnAlaGlyValIValSerTrpGIyGlu 220
 QY 667 GGCTGTGCCACCGCAACCGGCTGGCATCTACCCGCTGTACCTACTACTTGGACATGG 726
 |||||||
 DB 221 GlyCySAlaGlnPrAspAsnArPrGlyIleTyTrHrArGValIthTrTyTrLeuAspTrp 240
 QY 727 ATCCACCACTATGTCCCAAAAAAGCG 753
 |||||||
 DB 241 IIEHSHISITyValPrOlyslsPro 249
 RESULT 5
 AAU12011 standard: Protein: 249 AA.
 ID AAU12011
 AC AAU12011:
 XX 09-APR-2002 (first entry)
 DE Human beta-II tryptase active site mutant S194A #1.
 XX
 KM Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; mutlein.
 OS Homo sapiens.
 XX Synthetic.
 XX W0200198470-A2.
 PN
 XX 27-DEC-2001.
 PD
 XX 20-JUN-2001; 2001MO-US19681.
 PF
 XX 21-JUN-2000; 2000US-0598982.
 PR (PROM-) PROMEGA CORP.
 PA
 XX Maffit M, Niles AL, Haek-Frendscho M;
 PI WPI: 2002-114578/15.
 DR N-PSDB: AAS20777.
 XX
 XX DNA construct for producing enzymatically-inactive proteolytic
 PT tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PR an active site mutation -
 PS Claim 8; page 90-91; 126pp; English.
 XX
 XX The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The

CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II tryptase active site mutants.
 CC
 XX SQ Sequence 249 AA:
 Alignment Scores:
 Pred. No.: 6.86e-97 Length: 249
 Score: 1384.00 Matches: 247
 Percent Similarity: 99.60% Conservatve: 1
 Best Local Similarity: 99.20% Mismatches: 1
 Query Match: 94.92% Indels: 0
 DB: 23 Gaps: 0
 US-09-598-982-20 (1-771) x AAU12011 (1-249)
 QY 7 CTCGAGAAAAGAAATGCTGGGGGTGACAGAGGCCCCAGAGCAAGTGGCCCTGCAGGTG 66
 |||||||
 DB 1 LeuGIUlySArGIleValIyGlyGlnGlnAlaIProArGserIyTrPrOtrpGIValI 20
 QY 67 AGCCGTGAGATCCACGGCCCAATGAGATGCATCTCTGGGGGGCTCCCTCATCCACCCC 126
 |||||||
 DB 21 SerLeuArGValHisGlyPrOTrpTrpMetHisPheCySGLySerLeuIIEHISPro 40
 QY 127 CAGTGGGTGCTGACCGCCCGCGGCTGGGAGACCGGAGCTGAAGATGTGGCCGCTC 186
 |||||||
 DB 41 GlnTrpValLeuThrAlaIHisCysValGIyPrOAspValIlySPrOleuIAlaIleu 60
 QY 187 AGGTTGCANCTGCGGGAGCAGACCTCTACTACCAAGGACAGCTGCTGGCTGCAGCAG 246
 |||||||
 DB 61 ArgValGlnIleuArGIuGlnHisIleuTyTrGIAspGlnIleuPrOValISerArG 80
 QY 247 ATCATCTGTCACCCACAGTTCTPACACCCGCCAGATTCGAGCGACATCCGCCCTGTGAG 306
 |||||||
 DB 81 IIEIleValHisPrOgIInPheTyTrHrAlaGlnIIEGlyAlaAspIleAlaIleuGln 100
 QY 307 CTGGAGAGCCGGTGAAGTCTCCAGCCAGCTCCACAGCGGTACACCTGGCCCTGCTCA 366
 |||||||
 DB 101 LeuGIUlyGlnPrOValIlySValISerSerHisValHisTrHrValIthTrLeuPrOArISer 120
 QY 367 GAGACCTTCCCGCCCGGATGCTGGCTGGCTGCTGCTGGCGGATGTGGACAATGAT 426
 |||||||
 DB 121 GIUTrHrPhePrOgIyMetPrOcyStrpValIThrGIyTrpGlyAspValAspAsnAsp 140
 QY 427 GAGCGCCGCCACCGGCATTTCTCTGAAAGCAGGTGAAGTCCCATTAATGAAAACAC 486
 |||||||
 DB 141 GIUATrgLeuPrProPhroheProleuLysGlnValIyValProIleMetGIuansHis 160
 QY 487 ATTTGTGACGCAAAATFACCACTTGGCCCTTACAGGGGAGACAGCGATCGTCCGT 546
 |||||||
 DB 161 IIECySAspAlaIlystrHisLeuGlyAlaIyTrHrGlyAspAspValArGIlleValAag 180
 QY 547 GAGCAGATGCTGTGTGCCGGAACACCCCGAGGAGACTCATGCCAGGGGACATCCGAGGG 606
 |||||||
 DB 181 AspAspMetLeuCyAlaIyAsnHrArGArGAspSerCyGlnIyAspSerGIyGly 200
 QY 607 CCCCTGTGTGCAAGGTGAATGGCACCTGGCTGCAGAGCGGGCGGTGGCTGAGTGGCCGAG 666
 |||||||
 DB 201 ProLeuValIyLysValAsnGlyTrHrTrpLeuGlnAlaGlyValIValSerTrpGIyGlu 220
 QY 667 GGCTGTGCCACCGCAACCGGCTGGCATCTACCCGCTGTACCTACTACTTGGACATGG 726
 |||||||
 DB 221 GlyCySAlaGlnPrAspAsnArPrGlyIleTyTrHrArGValIthTrTyTrLeuAspTrp 240
 QY 727 ATCCACCACTATGTCCCAAAAAAGCG 753
 |||||||
 DB 241 IIEHSHISITyValPrOlyslsPro 249
 RESULT 6
 AAU12012 standard: Protein: 249 AA.
 ID AAU12012

PR DNA construct for producing enzymatically-inactive proteolytic
 PR trypsin, comprises DNA sequence encoding proteolytic trypsin having
 PR an active site mutation -
 PS Disclosure: Page 74-75; 126pp; English.
 XX
 XX
 CC The present invention relates to recombinant human proteolytic
 CC trypsin, active site mutants of these trypsin and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsin with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsin that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II trypsin. The active site mutants of proteolytic trypsin provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypsin produced are
 CC useful as an antigen to generate anti-human trypsin antibodies
 CC and in drug screening for compounds which act as trypsin inhibitors,
 CC antagonists, agonists, etc. The present sequence represents human
 CC beta-I trypsin.
 CC
 XX Sequence 249 AA:
 SQ
 Alignment Scores:
 Pred. No.: 9.72e-97 Length: 249
 Score: 1382.00 Matches: 247
 Percent Similarity: 99.20% Conservative: 0
 Best Local Similarity: 99.20% Mismatches: 2
 Query Match: 94.79% Indels: 0
 DB: 23 Gaps: 0
 US-09-598-982-20 (1-771) x AAU12006 (1-249)
 OY 7 CTCGAGAAAAGATCTCGGGGTCAGAGGCCCCAGGAGCAATGGCCCTGGCAGGTG 66
 DB 1 LGGILLYLARGIILEVALGILYGLNGILALAPROARGSERLYSTRPRORPRGILV 20
 OY 67 ACCCTGAGAGTCCAGCGCCCATRACGTGATGACATTTGGGGGGCTCCATGACCC 126
 DB 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyYSerLeuIleHisPro 40
 OY 127 CAGTGGGTCTGACCGCCGGGGGTGGTGGGAGCCGATCAAGGATGCGCCGCCCTC 186
 DB 41 GILTRVALLEIHTHALAALAHISCVSVALGILYPROASPVALLYSAPREUADAALALE 60
 OY 187 AGGTTGCAACTGCGGGAGCAGCACTCTACTACAGGAGCAGCCTGCTGGCGTCAAGG 246
 DB 61 ArgValGlnLeuAlaArgGlnGlnHisLeuYrTyrGlnAspGlnLeuLeuProValSerArg 80
 OY 247 ATCATGTCGACCCAGCATGTTTACACCGCCCGAGATGGAGCGGACATCGCCCTGGGAG 306
 DB 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyValAspIleAlaLeuLeuGln 100
 OY 307 CTGGAGAGCCGGTGAAGGTCTCCAGCCAGCTCCACAGCGTCAACCTGGCCCTGGCTGA 366
 DB 101 LeuGlnGlnProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer 120
 OY 367 GAGACCTTCCCGCCGGGAGTCCGCTGCTGCTACTGCTGGGGGCGATGGCAATGAT 426
 DB 121 GILTRPheProProGlyMetProCysTrpValThrGlyTrpGlyLysPValAspAsnAsp 140
 OY 427 GAGCGCTCCAGCCGCAATTTCTCTGAAGCAGAGTADAGTCCCAATATGAAAAACAC 486
 DB 141 GILTRPheProProGlyMetProCysTrpValThrGlyLysPValAspAsnAsp 160
 OY 487 ATTTGTGAGCAAAAATACACCTTGGCGCTACAGGGAGAGAGAGTCCGCAATGCTGGT 546
 DB 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValAsp 180
 OY 547 GAGGACATCTGTGTGTCGGGAAACACCCGAGGAGACTCATGCCAGGGCGACTCCGAGGG 606

DB 181 AspAspMetLeuCysAlaGlyLysnThrArgArgAspSerCysGlnGlySperGlyGly 200
 OY 607 CCCCTGGTGTGCAAGGTAAATGGACACCTGGCTGACAGCGGGCGGTGCTACGTTGGCGAG 666
 DB 201 ProLeuValCysLysValAsnGlyTrpTrpLeuGlnAlaGlyValAlaSerTrpGlyGln 220
 OY 667 GGGTGGCCAGGCCAAGCGGCTGGCANTCTACCCCGTCAACCTACCTACTGGAGCTGG 726
 DB 221 GILYSAIAGLInProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
 OY 727 ATCCACCACTATGCTCCCAAAAAGCCG 753
 DB 241 IleHisHisTyrValProLysLysPro 249
 RESULT 8
 AAU12010
 ID AAU12010 standard; Protein; 249 AA.
 XX
 AC AAU12010;
 XX
 DT 09-APR-2002 (First entry)
 XX
 XX Human beta-II trypsin active site mutant D91A #1.
 DE Human beta-II trypsin active site mutant D91A #1.
 DE Human beta-II trypsin active site mutant D91A #1.
 KW Human: proteolytic trypsin; protease; recombinant beta-II trypsin;
 KW enzyme; mutant; mutain.
 KW
 XX Homo sapiens.
 OS Synthetic.
 PN W0200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-US19681.
 XX
 PR 21-JUN-2000; 2000US-0598982.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Maffit M, Niles AL, Haak-Frendscho M;
 PI
 DR WPI: 2002-114578/15.
 DR N-PSDB: AAS20776.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PR trypsin, comprises DNA sequence encoding proteolytic trypsin having
 PR an active site mutation -
 PS Claim 8; Page 87-88; 126pp; English.
 XX
 XX The present invention relates to recombinant human proteolytic
 CC trypsin, active site mutants of these trypsin and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsin with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsin that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II trypsin. The active site mutants of proteolytic trypsin provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypsin produced are
 CC useful as an antigen to generate anti-human trypsin antibodies
 CC and in drug screening for compounds which act as trypsin inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II trypsin active site mutants.
 CC
 XX Sequence 249 AA:
 SQ
 Alignment Scores:
 Pred. No.: 9.72e-97 Length: 249
 Score: 1382.00 Matches: 247
 Percent Similarity: 99.20% Conservative: 0
 Best Local Similarity: 99.20% Mismatches: 2
 Query Match: 94.79% Indels: 0
 DB: 23 Gaps: 0

Pred. No.: 1.64e-96 Length: 249
 Score: 1379.00 Matches: 247
 Percent Similarity: 99.20% Conservative: 0
 Best Local Similarity: 99.20% Mismatches: 2
 Query Match: 94.58% Indels: 0
 DB: 23 Gaps: 0

US-09-598-982-20 (1-771) x AAU12019 (1-249)
 QY 7 CTCGAGAAAAGATGTCGGGGGTCAGAGAGGCCCCAGAGGAAAGTGGCCCTGGCAGGTC 66
 DB 1 LeuGluLysAlaGlnLeuValGlyGlnGlnGlnAlaProAlaGlySerLysTrpProTrpGlnVal 20
 QY 67 AGCCGTGAGTCCAGCGCCGCATCTGATGCACTTCTGGGGGGCTCCCTCATCCAGCC 126
 DB 21 SerLeuAlaGlyValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
 QY 127 CAGTGGGTGTCGACCGCCGGCGGCTGGCGGAGCCGAGAGTCAAGATGTGGCCGCTC 186
 DB 41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaIleu 60
 QY 187 AGGGTGAACGTGGGAGAGCAGCTTACTACGACCTTACTGACGAGCCAGTGGCTGGCGAGG 246
 DB 61 ArgValGlnLeuAlaArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArg 80
 QY 247 ATCATGTGTCACCCAGTCTTACACCGCCGCAGATCGAGCGAGCATCGCCCTGGTGGAG 306
 DB 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAlaIleIleAlaLeuGln 100
 QY 307 CTGGAGGAGCGGGTAAAGTGTCTCCAGCCAGCTCCACAGAGGTGACCCCTGGCCCTGCA 366
 DB 101 LeuGlnGluProValLysValSerHisValHisThrValThrLeuProProAlaSer 120
 QY 367 GAGACCTTCCCGCCGGGAGTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
 DB 121 GlnTrpPheProProGlyMetProCysTrpValIleThrGlyTrpGlyAspValAspAsnAsp 140
 QY 427 GAGCGCCCTCCAGCCGCATCTCTGTAAGCAGAGGTGAAGGTCCTCCATAATGAAAAAC 486
 DB 141 GluAlaGluProProPheProPheProLeuLysGlnValLysValProIleMetGlnAsnHis 160
 QY 487 ATTTGTGACGGCAAAATACCACTTGGCCGCTTACAGCGGAGAGAGAGAGAGAGAGAGAG 546
 DB 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspAlaArgIleValAla 180
 QY 547 GAGCAGATCTGTGTCGGGAGAACCCGGAGGAGACTATCCAGCGGAGCTCCGGAGGG 606
 DB 181 AspAspMetLeuCysAlaGlnAsnTrpArgAspSerCysGlnGlyAspSerGlyGly 200
 QY 607 CCCCTGGTGTGCAAGGTGAATGCGACCTGGCTGCGAGCGCGGCTGCACTGGGGCGAG 666
 DB 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValAlaSerTrpGlyGln 220
 QY 667 GGCTGTGGCCAGCCAGCGGCTGGCATCTACCCGGTGCACCCGATCACTTGGAGCTGG 726
 DB 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
 QY 727 ATCCACCACTATGTCGCCAAAAAGCCG 753
 DB 241 IleHisHisTyrValProLysLysPro 249
 RESULT 9
 AAU12019
 ID AAU12019 standard: Protein: 249 AA.
 AC AAU12019;
 AC AAU12019;
 DT 09-APR-2002 (first entry)
 XX Human beta-II tryptase active site mutant S194A #5.
 DE Human beta-II tryptase active site mutant S194A #5.
 XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; mutain.

XX XX Homo sapiens.
 OS Synthetic.
 XX XX WO200198470-A2.
 PN 27-DEC-2001.
 PD 20-JUN-2001; 2001WO-US19681.
 PE 21-JUN-2000; 2000US-0598982.
 PR (PROM-) PROMEGA CORP.
 PA Matfit M, Miles AL, Haak-Frendscho M;
 PI MPI: 2002-114578/15.
 DR N-PSDB: AAS20785.
 DR DNA construct for producing enzymatically-inactive proteolytic
 PR tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PT an active site mutation
 PS Claim 8; Page 111-112; 126pp; English.
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzyme is an antigen, recombinant proteolytic tryptase antibodies
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II tryptase active site mutants.
 XX XX Sequence 249 AA:
 SQ
 Alignment Scores:
 Pred. No.: 1.64e-96 Length: 249
 Score: 1379.00 Matches: 246
 Percent Similarity: 99.20% Conservative: 1
 Best Local Similarity: 98.80% Mismatches: 2
 Query Match: 94.58% Indels: 0
 DB: 23 Gaps: 0
 US-09-598-982-20 (1-771) x AAU12019 (1-249)
 QY 7 CTCGAGAAAAGATGTCGGGGGTCAGAGAGGCCCCAGAGGAAAGTGGCCCTGGCAGGTC 66
 DB 1 LeuGluLysAlaGlnLeuValGlyGlnGlnGlnAlaProAlaGlySerLysTrpProTrpGlnVal 20
 QY 67 AGCCGTGAGTCCAGCGCCGCATCTGATGCACTTCTGGGGGGCTCCCTCATCCAGCC 126
 DB 21 SerLeuAlaGlyValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
 QY 127 CAGTGGGTGTCGACCGCCGGCGGCTGGCGGAGCCGAGAGTCAAGATGTGGCCGCTC 186
 DB 41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaIleu 60
 QY 187 AGGGTGAACGTGGGAGAGCAGCTTACTACGACCTTACTGACGAGCCAGTGGCTGGCGAGG 246
 DB 61 ArgValGlnLeuAlaArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArg 80
 QY 247 ATCATGTGTCACCCAGTCTTACACCGCCGCAGATCGAGCGAGCATCGCCCTGGTGGAG 306

Db 81 ILeIleValHIsPrOgInPheRyTrHraLaGInIleGlyAlaSpRleAlaLeuGIn 100
 QY 307 CTGAGAGACCCGGTAAAGGTTCTCAAGCCACGTCACAGCGTACCCCTGCCCTGCCCTCA 366
 Db 101 LeuGIuGIuPrOvAlAsnValSerSerHisValHisThrValThrLeuPrOroAlaSer 120
 QY 367 GAGACCTTCCCGCCGGGATGCGCGTGGTCACTGGCTGGGGCGATGTGACAAATGAT 426
 Db 121 GIuTrHrPhePrOroGIuMeTrProCysTrPValThrGIuTrPGLyAsPValAspAsnAsp 140
 QY 427 GAGCGCCCTCCCAACCGCATTTCTCTGAAGCAGGTGAAGGTCCTCCCAATGAAAAACCC 486
 Db 141 GIuATGLeuPrOroPrOroPhePrOleuLysGIuValIlyValPrOleMeTGIuAsnHis 160
 QY 487 ATTTGTGACGCAAAATATCACCTTGGCGCTACAGCGGAGACGAGTCCGATCGCTCGT 546
 Db 161 ILeCysAsPAlaIlySTyrlHisIleuGIuAlaYrTrHrGIuAsPAsPValAlaArgIleValAla 180
 QY 547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGACTATGCCAGGGCGACTCCGGAGGG 606
 Db 181 AspAspMeTLeuCysAlaIaGIuAsnTrHrArGArGAsPSeRcYsGIuIaGlyAlaGIu 200
 QY 607 CCCCTGGTGTGAAAGTGAATGGCACTGTGGTCAAGCGGGCGTGTCACTGGGGCGAG 666
 Db 201 PrOleuValCysIlySValAsnGIuTrHrPrLeuGIuAlaGIuValIlyValSerTrPGLyGIu 220
 QY 667 GGCTGTGCCACCCCAACCGCGCTGGCATCTACACCCGTGTCACCTACTTGGACTGG 726
 Db 221 GIuCYsAlaGIuPrOroAsnArgPrOroGIuIleYrTrHrArGIuValThrTrYrIleuAsPTrP 240
 QY 727 ATGCACCACTATGTCCCAAAAAAGCGG 753
 Db 241 ILeHisIlySTyrlPrOlySTySPrO 249
 RESULT 10
 AAU12020
 ID AAU12020 standard; Protein: 249 AA.
 AC AAU12020;
 XX 09-APR-2002 (first entry)
 DE Human beta-II tryptase active site mutant S194A #6.
 KM Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KN enzyme; mutant; mutain.
 OS Homo sapiens.
 OS Synthetic.
 OS WO200198470-A2.
 PN 27-DEC-2001.
 PD 20-JUN-2001; 2001WO-US19681.
 PF 21-JUN-2000; 2000US-0598982.
 PR (PROM-) PROMEGA CORP.
 PA (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI: 2002-114578/15.
 DR N-PSDB: AAS20786.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT trypase, comprises DNA sequence encoding proteolytic trypase having
 PT an active site mutation -
 XX
 PS Claim 8: Page 114-115; 126pp; English.
 CC The present invention relates to recombinant human proteolytic
 CC trypases, active site mutants of these trypases and the methods for

CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypase with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-inactive
 CC beta-II trypase. The active site mutants of proteolytic trypase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypase produced are
 CC useful as an antigen for generate anti-human trypase antibodies
 CC and in drug screening for compounds which act as trypase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II trypase active site mutants.
 SQ Sequence 249 AA:
 Alignment Scores:
 Pred. No.: 1.64e-96 Length: 249
 Score: 1379.00 Matches: 246
 Percent Similarity: 99.20% Conservative: 1
 Best Local Similarity: 98.80% Mismatches: 2
 Query Match: 94.58% Indels: 0
 DB: 23 Gaps: 0
 US-09-598-982-20 (1-771) x AAU12020 (1-249)
 QY 7 CTGAGAAAAAATGTCGGGGGTCAAGAGCCCCCAAGGACAAAGTGGCCGACAGTGG 66
 Db 1 LeuGIuLysArgIleValGIuGIuInGIuAlaPrOroArgSerLysTrPrOroTrPGLyAl 20
 QY 67 AGCCGTGAGTCCACAGGCCCATACTGATGATGATGATCTGTGGGGGGCCCTCCATPCACACCC 126
 Db 21 SerLeuAlaGValHisGIuPrOroTrYrPwEchHisPheCysGIuIlySerLeuIleHisPro 40
 QY 127 CAGTGGTCCCTGACCCCGCCGCGCTGGGAGCCGACGTCAGAGATCTGGCCCGCTTC 186
 Db 41 GIuTrPValIleuThrAlaIleHisCysValGIuPrOAsPValIlyAsPValAlaIleu 60
 QY 187 AGGGTGAACCTGGGGAGAGACACTCTACTACAGAGACCACTGCTGGCGGTCAAGCAGG 246
 Db 61 ArgValGIuIleuAlaArgGIuInGIuHisIleuTrYrGIuAsPGIuIleuPrOValSerArg 80
 QY 247 ATCATGTGTCACCCACAGTTCATCAACCCGCCGATCCGAGCGGACATGCCCTGGTGGAG 306
 Db 81 ILeIleValHIsPrOgInPheRyTrHraLaGInIleGlyAlaAsPLeIAlaLeuGIn 100
 QY 307 CTGAGAGACCCGGTAAAGGTTCTCAAGCCACGTCACAGCGTACCCCTGCCCTGCCCTCA 366
 Db 101 LeuGIuGIuPrOvAlAsnValSerSerHisValHisThrValThrLeuPrOroAlaSer 120
 QY 367 GAGACCTTCCCGCCGGGATGCGCGTGGTCACTGGCTGGGGCGATGTGACAAATGAT 426
 Db 121 GIuTrHrPhePrOroGIuMeTrProCysTrPValThrGIuTrPGLyAsPValAspAsnAsp 140
 QY 427 GAGCGCCCTCCCAACCGCATTTCTCTGAAGCAGGTGAAGGTCCTCCCAATGAAAAACCC 486
 Db 141 GIuATGLeuPrOroPrOroPhePrOleuLysGIuValIlyValPrOleMeTGIuAsnHis 160
 QY 487 ATTTGTGACGCAAAATATCACCTTGGCGCTACAGCGGAGACGAGTCCGATCGCTCGT 546
 Db 161 ILeCysAsPAlaIlySTyrlHisIleuGIuAlaYrTrHrGIuAsPAsPValAlaArgIleValAla 180
 QY 547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGACTATGCCAGGGCGACTCCGGAGGG 606
 Db 181 AspAspMeTLeuCysAlaIaGIuAsnTrHrArGArGAsPSeRcYsGIuIaGlyAlaGIu 200
 QY 607 CCCCTGGTGTGAAAGTGAATGGCACTGTGGTCAAGCGGGAGACGAGTCCGATCGCTCGT 666
 Db 201 PrOleuValCysIlySValAsnGIuTrHrPrLeuGIuAlaGIuValIlyValSerTrPGLyGIu 220
 QY 667 GGCTGTGCCACCCCAACCGCGCTGGCATCTACACCCGTGTCACCTACTTGGACTGG 726

Db 221 GYCSYSLAGLmProAsnArgrProGlyIleTyrThrArgValThrTyrTyrLeuAsprr 240
 QY 727 ATCCACACTATGTCGCCCAAAAAGCCG 753
 Db 241 IIEHSHSTYrValProLysLysPro 249

RESULT 11
 AAU12013
 ID AAU12013 standard: Protein: 245 AA.

AC AAU12013:
 DT 09-APR-2002 (first entry)
 DE Human beta-II tryptase active site mutant H44A #2.

KN Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; mutain.
 XX Homo sapiens.
 OS Synthetic.

OS MO200198470-A2.
 PN MO200198470-A2.
 XX 27-DEC-2001.
 PD 20-JUN-2001; 2001MO-US19681.

PF 21-JUN-2000; 2000US-0598982.
 XX (PROM-) PROMEGA CORP.
 PA Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI: 2002-114578/15.
 DR N-PSDB; AAS20779.

PI DNA construct for producing enzymatically-inactive proteolytic
 PT tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PR an active site mutation -
 XX Claim 40; page 95-96; 126pp; English.

CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modeling studies. The
 CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II tryptase active site mutants.

CC Sequence 245 AA;
 S0

Alignment Scores:
 Pred. No.: 3.92e-96 Length: 245
 Score: 1374.00 Matches: 245
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.24% Indels: 0
 DB: 23 Gaps: 0

US-09-598-982-20 (1-771) x AAU12013 (1-245)

QY 19 ATCTGCGGGGCTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGAGGCTGAGAGTC 78
 Db 1 IIEVAlGIGLgYngLqUAlarProArgrSerLysrPrroTrrpGlnValSerLeuArGVal 20

QY 79 CAGGCCCCATPACTGGATGCACCTTGGCGGGGCTCCATCCACCCCACTGGGTGCTG 138
 Db 21 HISSGlyProTyrTrpMetHisPhecysgIySerLeuIleHisProGlnTrpValLeu 40

QY 139 ACCGGCGGGGCTGGGAGCCGAGCCAGGATGTCGAGGATGTCGAGGATGTCGAG 198
 Db 41 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArGValGlnLeu 60

QY 199 CCGAGAGCAAGCACTTACTACCCAGAGCCAGCTGCTGCCGTCAGAGGATCATCCGTCAC 258
 Db 61 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80

QY 250 CCAAGATTCTACAGCCGCCAGATGGAGCGGACATGCCCTGCTGGAGCTGGAGAGCCG 318
 Db 81 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuGlnGlnIlePro 100

QY 319 GTGAAGGTCCTCCAGCCAGCTCCACAGCGGTCAACCCGTCGCGCCCTCAAGAGCTTCCCC 378
 Db 101 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGlnThrPhePro 120

QY 379 CCGGGGATGCTCCGCTGGGTCACCTGGCTGGGCGAGTGTGAGACATGATGAGCCCTCCCA 438
 Db 121 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGlnArGLeuPro 140

QY 439 CCGCCATTTCTCTGAAAGCAAGGTCCCAATGAAACACACATTTGTGACGCA 498
 Db 141 ProporpheroleuLysGlnValLysValProIleMetGlnHisHisIleCysAspAla 160

QY 499 AATATCCACCTGGGCGCTACACGGGAGAGAGGATGCCGATGCCGTCAGCAGCATMGCTG 558
 Db 161 LysTyrHisLeuGlyAlaLysThrLysAspAspValAlaGlyLeuAlaLysAspMetLeu 180

QY 559 TGTGCCGGGAACACCCCGGAGGACTCANGCCAGGGCGACTCCGAGGGCCCTGGTGTGC 618
 Db 181 CysAlaGlyAsnThrArgArGAspSerCysGlnGlyAspSerClyGlyProLeuValCys 200

QY 619 AAGTGAATGGCACTGGCTGAGCGGGCGGTGTACAGCTGGGGCGAGAGGCTGTGCCAG 678
 Db 201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValIleSerTrpGlyGlnGlyCysAlaGln 220

QY 679 CCCAACCGGCGGATGTCACACCCGTCACCTTACTTGGACTGGATCCACCACTAT 738
 Db 221 ProAsnArGProGlyIleTyrThrArGValThrTyrTyrLeuAspTrpIleHisIlyr 240

QY 739 GTCCCCAAAAGCCG 753
 Db 241 ValProLysLysPro 245

RESULT 12
 AAU12018
 ID AAU12018 standard: Protein: 249 AA.

AC AAU12018:
 DT 09-APR-2002 (first entry)
 DE Human beta-II tryptase active site mutant D91A #3.

KN Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; mutain.
 XX Homo sapiens.
 OS Synthetic.
 OS MO200198470-A2.
 PN 27-DEC-2001.
 PD

US-09-598-982-20 (1-771) x AAU12013 (1-245)

PF 20-JUN-2001; 2001WO-US19681.
 XX
 PR 21-JUN-2000; 2000US-0598982.
 XX
 XX (PROM-) PROMEGA CORP.
 XX
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX
 DR MPI: 2002-114578/15.
 DR N-PSDB: AAS20784.

PF DNA construct for producing enzymatically-inactive proteolytic
 PR trypsinase, comprises DNA sequence encoding proteolytic trypsinase having
 PI an active site mutation -
 XX
 XX
 PS Claim 8; Page 109-110; 126pp; English.

CC The present invention relates to recombinant human proteolytic
 CC trypsinases, active site mutants of these trypsinases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsinase with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsinase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-inactive
 CC beta-II trypsinase. The active site mutants of proteolytic trypsinase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypsinase produced are
 CC useful as an antigen to generate anti-human trypsinase antibodies
 CC and in drug screening for compounds which act as trypsinase inhibitors,
 CC antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
 CC human beta-II trypsinase active site mutants.
 XX
 XX Sequence 249 AA:

5Q Alignment Scores:
 Pred. No.: 3,93e-96 Length: 249
 Score: 1374.00 Matches: 246
 Percent Similarity: 98.80% Conservative: 0
 Best Local Similarity: 98.80% Mismatches: 3
 Query Match: 94.24% Indels: 0
 DB: 23 Gaps: 0

US-09-598-982-20 (1-771) x AAU12018 (1-249)

QY 7 CTCGAGAAAAGATGTCGGGGGTCAGAGAGCCCGCAGAGCAAGTGGCCCTGGCAGTGG 66
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 LeuGIuLylsArIRIIleValGIyGInGIuAlaProArGylsrrProrIrrpGIInVal 20
 QY 67 AGCCGTGAGAGTCCAGCGCCCACTAGATGATGATGATGATGATGATGATGATGATGAT 126
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 21 SerLeuArGValAHISGIYPrOTYrTrrPmEThISpHeCySGIYGIYSerLeuIleHISPrO 40
 QY 127 CAGTGGGmGTACCGC 186
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 41 GIuTrPrValLeuThrAlaAlaHIScYsValGIYPrOArSValIlySpLeuAlaAlaLeu 60
 QY 187 AGGGTGCACATCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 246
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ArgValGIuLeuArGIuGIuInHISLeuYrYrGIuInAsPGIuLeuIleuArGIuSerArg 80
 QY 247 ATCATGCTGCACCCACAGTTCATACACCGCCCGCAGATCGAGCGGACATCGCCCTGGTGGAG 306
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 81 IIEIleValAHISPrOInHeYrThrAlaGIInIleGIYAlaAlaIleAlaLeuLeuGIu 100
 QY 307 CTGGAGGAGCCGGTGAAGGTTCACGCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 366
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 101 LeuGIuGIuPrOValAsnAlSerSerHISrValHISrHValIthreuPrOArIaSer 120
 QY 367 GAGACCTTCGCCCGGGAGTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 426
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 GIuTrPrHePrOPrOGLyMeTPrOCysTrPrValIThrGIYTrPrGIYAsPrValAsPAsnAsP 140
 QY 427 GAGCGCCCTCCCGCCGCAATTCCTCTGAAAGCAGGTGAAGTCCCATATGAAAAACAC 486
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 141 GIuArGIuPrOPrOHePrOHePrOHePrOHePrOHePrOHePrOHePrOHePrOHePrO 160
 QY 487 ATTTGTGACGCAAAAATPACCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 546
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 161 IIEcYsAsPrAlDylsTYrHISLeuGIYAlaIYrThrGIYAsPrAsPrAlDylsValArg 180
 QY 547 GACGACATGCTGTGTGCCCGGGAACCGCGGAGGAGCAGTCCAGCGCGCGCGCGCGCG 606
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AspAsPmELeuCYsAlaGIuYsAlaInGIYrThrPrLeuGIuAlaGIYValIleSerIrrpGIu 200
 QY 607 CCCCCTGGTGGAGGTGAATGGCACCTGGCTGCAGGCGCGCGCGTGTACGTGGGGCGAG 666
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 201 PrOLeuValCYsIlysValAsnGIYrThrPrLeuGIuAlaGIYValIleSerIrrpGIu 220
 QY 667 GGCCTGGCCCGCCAGCG 726
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 221 GIYCYsAlaGIuPrOArSArGIYIleYrThrArGIuValIthrTYrIleuAsPrIrr 240
 QY 727 ATCCACACTATGTCGCCCAAAAAGCGG 753
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 IIEHISHSISrYrValPrOlySlySPrO 249

RESULT 13
 AAU12021
 ID AAU12021 standard; Protein; 245 AA.
 XX
 XX AAU12021;
 AC
 XX
 DT 09-APR-2002 (first entry)
 XX
 XX Human beta-II trypsinase active site mutant H44A #4.
 DE
 XX
 KW Human: proteolytic trypsinase; protease; recombinant beta-II trypsinase;
 KW enzyme; mutant; mutain.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200198470-A2.
 XX
 PD 27-DEC-2001.
 PF
 XX
 XX 20-JUN-2001; 2001WO-US19681.
 XX
 XX 21-JUN-2000; 2000US-0598982.
 PR
 XX
 PA (PROM-) PROMEGA CORP.
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX
 DR MPI: 2002-114578/15.
 DR N-PSDB: AAS20787.
 XX
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT trypsinase, comprises DNA sequence encoding proteolytic trypsinase having
 PI an active site mutation -
 XX
 XX
 PS Claim 40; Page 117-118; 126pp; English.

CC The present invention relates to recombinant human proteolytic
 CC trypsinases, active site mutants of these trypsinases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsinase with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsinase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-inactive
 CC beta-II trypsinase. The active site mutants of proteolytic trypsinase provide


```
OY 139 ACCGCCGCGCTGCGTGGGACCAGCACTCAAGATCTGGCCGCGCCAGGCTGCNACTG 198
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 41 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 60
OY 199 CGGAGCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 258
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 61 ArgGlnGlnHisLeuTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80
OY 259 CCACAGTCTTACACAGCCAGATCCGAGAGCAATCCGCCCCCTGGAGAGCGGCCG 318
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 81 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 100
OY 319 GTGAAGGTCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 378
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 101 ValLysValSerSerHisValHisThrValIleuLeuProProLaseGlnuThrPhePro 120
OY 379 CCGGAGATCCGCTGTGGGTCAGCTGGCGGCGGATGTGGACAAATGATGAGCCCTCCCA 438
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 121 ProGlyMetProCysTrpValIleThrGlyTrpGlyAspValAspAsnAspGlnuArgLeuPro 140
OY 439 CCGCCATTCTCTGAGGAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 498
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 141 ProProPheProLeuLysGlnValLysValProIleMetGlnAsnHisIleCysAspAla 160
OY 499 AATATACACACTTGGCGCCTAACAGCGGAGGAGAGCAAGCTCCGATGCTCGGTGAGCATGCTG 558
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 161 LysTyrHisLeuGlyAlaIleArgIleArgIleValIleValIleArgIleValIle 180
OY 559 TGTGGCCGGAAACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 618
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 181 CysAlaIleGlyAsnIleArgIleArgIleValAspSerCysGlnIleGlyProLeuValCys 200
OY 619 AAGGTGAATGGACAGCCTGGCTGACAGGGGGCGCTGGTACGCTGGGGCGGAGGGCTGTCCCGCA 678
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpIleGlyCysAlaGln 220
OY 679 CCCAACCCGCGCTGGATCTAACACCCGCTGACCTACTACTGATGGAGTCCAGCACTAT 738
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 221 ProAsnArgProGlyIleuArgValIleIleThrTrpLeuAspTrpIleHisIle 740
OY 739 GTCCCGCAAAAAGCCG 753
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 241 ValProLysLysPro 245
RESULT 15
AAM64240
ID AAM64240 standard; Protein: 274 AA.
XX
AC AAM64240:
XX
XX 24-NOV-1998 (first entry)
DT
XX
DE Human mast cell tryptase II/beta.
XX
KW Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7;
KM blood clot; anticoagulant; myocardial infarction; reocclusion;
KW thromboembolism; cerebral embolism; thrombosis; therapy.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Sig_peptide
FT /label= 19..28
FT Peptide 19..28
FT /label= Pro_peptide
FT Protein 29..274
FT /label= Mat_protein
XX
PN MO9824886-A1.
XX 11-JUN-1998.
XX
```

```
PF 25-NOV-1997; 97WO-US21620.
XX
PR 04-DEC-1996; 96US-0032354.
XX
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI Stevens RL.
XX
DR WPI: 1998-333308/29.
DR N-PSDB: AAV44330.
XX
XX New compositions containing tryptase-7, e.g. mouse mast cell
PT Protease-7 - are used to treat clot formation in e.g. myocardial
PT infarction, reocclusion following angioplasty or pulmonary
PT thromboembolism
XX
PS Disclosure: Page 66-67; 92pp; English.
XX
XX This is the deduced amino acid sequence of human mast cell tryptase
CC II/beta (see also AAV44330). The invention provides: compositions
CC comprising an isolated tryptase-7 that may include chimeric proteins
CC that contain (a) a human tryptase for all but the active site region
CC and (b) the substrate-binding pocket of mouse tryptase-7 or its
CC homologues (see AAM64233-39); a method for treating a blood clot by
CC administering a nucleic acid molecule that codes for a tryptase-7,
CC or an expression product, to decrease fibrinogen activity; a nucleic
CC acid encoding a serine protease (SP) and a method of producing a
CC mature SP by expressing the inactive zymogen in a host cell, and
CC cleaving the enterokinase susceptibility domain. The tryptase-7
CC polypeptides can be used to treat disorders mediated by undesirable
CC thrombus clot formation such as myocardial infarction and
CC reocclusion following angioplasty of blood clots associated with
CC pulmonary thromboembolism, deep vein thrombosis, cerebral embolism,
CC renal vein and peripheral arterial thrombosis. They are also
CC useful for all surgical procedures that require decreased blood
CC clots.
XX
XX SQ sequence 274 AA:
Alignment Scores:
Pred. No.: 1,13e-95 Length: 274
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 2
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 93.83% Indels: 0
DB: Gaps: 0
US-09-598-982-20 (1-771) x AAM64240 (1-274)
OY 19 ATGCTGGGGGTRCAGAGGAGCGCCAGAGCAAGTGGCCCTGGAGGCTGAGACTG 78
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 30 IleValGlyGlnGlnLalaProArgSerLysTrpProTrpGlnValSerLeuAlaGVal 49
OY 79 CAGCGCCCATACTGTGATGACATCTGCGGGGGCTCCCTCATCCAGGCCAGTGGGCTG 138
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 50 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 69
OY 139 ACCGCCGCGCGTGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 198
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 70 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaIleuArgValGlnLeu 89
OY 199 CCGGAGCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 258
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 90 ArgGlnGlnHisLeuTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 109
OY 259 CCACAGTCTTACACAGCCAGATCCGAGAGCAATCCGCCCCCTGGAGAGCGGCCG 318
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 110 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaIleuLeuGluGluPro 129
OY 319 GTGAAGGTCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 378
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 130 ValLysValSerSerHisValHisThrValIleuLeuProProLaseGlnuThrPhePro 149
```

```

QY 379 CCGGGGATGCCGTGGTGGCTCACTGGCTGGGGGATGTGACAAATGATGAGCCCTCCCA 438
    |||
Db 150 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 169
    |||
QY 439 CCGCCATTTCTCTGTAGACAGGTGAAGTCCCATTAATGGAAAACACATTTGTGACGCA 498
    |||
Db 170 ProProPheProLeuIysGlnValIysValProIleMetGluAsnHisIleCysAspAla 189
    |||
QY 499 AAATACCACTTGGGGCCCTACACAGGGAGACAGTCCGATGCTGACGACATGCTG 558
    |||
Db 190 LysTyrHisLeuGlyAlaIleThrGlyAspAspValArgIleValIleArgAspAspMetLeu 209
    |||
QY 559 TGTGCCGGGACACCCCGAGGAGACTCATGACCAGGGGACTCCGAGGGCCCTGGTGTGC 618
    |||
Db 210 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 229
    |||
QY 619 AAGGTGAATGGCACTGGCTGCAAGGGCGGTGTGACGCTGGGGCGAGGGCTGTGCCAG 678
    |||
Db 230 LysValAsnGlyThrTrpLeuGlnAlaGlyValIleSerTrpGlyGlnGlyCysAlaGln 249
    |||
QY 679 CCCAACCCGGCTGGCATTCACACCCGCTGTACCTACTACTGGAGCTGATCCACCACTAT 738
    |||
Db 250 ProAsnArgProGlyIleTyrThrArgValIleTyrTrpLeuAspTrpIleHisHisTyr 269
    |||
QY 739 GTCCCCAAAAAGCCG 753
    |||
Db 270 ValProLysLysPro 274
    |||

```

Search completed: January 31, 2003, 06:53:08
 Job time : 59 secs

APD

Gencore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2003, 06:54:15 : Search time 31 Seconds
(without alignments)
1003.720 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 1458

Sequence: 1 gggcccccgcgagaagaat.....cgtgaagcggccgcctcgt 771

Scoring table:
BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 122226 segs, 20178551 residues

Total number of hits satisfying chosen parameters: 244452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlh
-CGN2_1/USPTO_pool/US05958982/runat_27012003_073718_19634/app_query.fasta_1.967
-DB=Published_Applications_AA -GFM=fastan -SUFFIX=n2p.rapp -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=-1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR.SCORE=pcct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFWT=ptc -NORM=ext -HEARSTIE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US05958982_qcgn_1_1_3_@runat_27012003_073718_19634
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEROUT=120 -WARN_TIMEROUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCRT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/US07_PUBCCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/PCRTS_PUBCCOMB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US10_PUBCCOMB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubppa/US60_PUBCCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608.5	41.7	311	US-09-900-754-2	Sequence 2, Appli
2	569.5	39.1	288	US-09-888-615-115	Sequence 115, App
3	563.5	38.6	290	US-10-041-006A-7	Sequence 7, Appli
4	563.5	38.6	290	US-10-028-072-222	Sequence 222, App

ALIGNMENTS

RESULT 1	US-09-900-754-2	Application US/09900754	Sequence 2, Appli	US-10-040-655-7	Sequence 7, Appli
5	563.5	38.6	290	12	US-10-040-655-7
6	554.5	38.0	315	9	US-10-041-006A-9
7	554.5	38.0	315	12	US-10-040-655-9
8	536.5	36.8	284	12	US-10-041-400A-7
9	536.5	36.8	284	12	US-10-041-264A-7
10	536.5	36.8	284	12	US-10-042-091A-7
11	527.5	36.2	316	12	US-10-041-400A-9
12	527.5	36.2	316	12	US-10-041-264A-9
13	527.5	36.2	316	12	US-10-042-091A-9
14	512	35.1	343	10	US-09-948-094-2
15	504.5	34.6	238	9	US-10-067-761-19
16	504.5	34.6	238	10	US-09-804-156-19
17	501.5	34.4	317	9	US-09-905-291A-263
18	501.5	34.4	317	9	US-10-040-803-7
19	501.5	34.4	317	9	US-09-902-853-263
20	501.5	34.4	317	9	US-09-902-853-263
21	501.5	34.4	317	9	US-09-907-824-263
22	501.5	34.4	317	9	US-09-907-841-263
23	501.5	34.4	317	9	US-09-904-011-263
24	501.5	34.4	317	10	US-09-909-330-263
25	501.5	34.4	317	10	US-09-909-088B-263
26	501.5	34.4	325	10	US-09-908-711-114
27	501.5	34.4	325	10	US-09-764-898-278
28	499.5	34.3	322	10	US-09-764-898-207
29	494	33.9	314	9	US-09-905-291A-257
30	494	33.9	314	9	US-09-902-853-257
31	494	33.9	314	9	US-09-907-824-257
32	494	33.9	314	9	US-09-907-841-257
33	494	33.9	314	9	US-09-904-011-257
34	494	33.9	314	10	US-09-909-330-257
35	494	33.9	314	10	US-09-885-441-14
36	494	33.9	314	10	US-09-909-088B-257
37	492.5	33.8	327	9	US-10-040-803-8
38	477.5	32.8	818	10	US-09-888-615-111
39	476	32.6	453	9	US-09-978-295A-69
40	476	32.6	453	9	US-09-978-697-69
41	476	32.6	453	9	US-09-978-197A-69
42	476	32.6	453	9	US-09-999-832A-69
43	476	32.6	453	9	US-09-978-189-69
44	476	32.6	453	9	US-10-174-590-64
45	476	32.6	453	9	US-10-176-758-64

US-09-900-754-2
: Sequence 2, Application US/09900754
: Patent No. US20020026654A1
GENERAL INFORMATION:
: APPLICANT: Allen, Keith D.
: APPLICANT: Leviten, Michael W.
: TITLE OF INVENTION: TRANSGENIC MICE CONTAINING TRYPTASE GENE
: FILE OF INVENTION: DISRUPTIONS
: FILE REFERENCE: R-372
: CURRENT APPLICATION NUMBER: US/09/900,754
: CURRENT FILING DATE: 2001-07-06
: PRIOR APPLICATION NUMBER: US 60/216,109
: PRIOR FILING DATE: 2000-07-06
: PRIOR APPLICATION NUMBER: US 60/223,172
: PRIOR FILING DATE: 2000-08-07
: PRIOR APPLICATION NUMBER: US 60/244,111
: PRIOR FILING DATE: 2000-10-26
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 2
: LENGTH: 311
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-900-754-2
Alignment Scores: 5.56e-33 Length: 311

? PRIOR APPLICATION NUMBER: 60/063127
 ? PRIOR FILING DATE: 1997-10-24
 ? PRIOR APPLICATION NUMBER: 60/063327
 ? PRIOR FILING DATE: 1997-10-27
 ? PRIOR APPLICATION NUMBER: 60/063329
 ? PRIOR FILING DATE: 1997-10-27
 ? PRIOR APPLICATION NUMBER: 60/063550
 ? PRIOR FILING DATE: 1997-10-28
 ? PRIOR APPLICATION NUMBER: 60/063561
 ? PRIOR FILING DATE: 1997-10-28
 ? PRIOR APPLICATION NUMBER: 60/063704
 ? PRIOR FILING DATE: 1997-10-29
 ? PRIOR APPLICATION NUMBER: 60/063733
 ? PRIOR FILING DATE: 1997-10-29
 ? PRIOR APPLICATION NUMBER: 60/063735
 ? PRIOR FILING DATE: 1997-10-29
 ? PRIOR APPLICATION NUMBER: 60/063738
 ? PRIOR FILING DATE: 1997-10-29
 ? PRIOR APPLICATION NUMBER: 60/063755
 ? PRIOR FILING DATE: 1997-10-17
 ? PRIOR APPLICATION NUMBER: 60/064248
 ? PRIOR FILING DATE: 1997-11-03
 ? PRIOR APPLICATION NUMBER: 60/064809
 ? PRIOR FILING DATE: 1997-11-07
 ? PRIOR APPLICATION NUMBER: 60/065186
 ? PRIOR FILING DATE: 1997-11-12
 ? PRIOR APPLICATION NUMBER: 60/065846
 ? PRIOR FILING DATE: 1997-11-17
 ? PRIOR APPLICATION NUMBER: 60/066364
 ? PRIOR FILING DATE: 1997-11-21
 ? PRIOR APPLICATION NUMBER: 60/066453
 ? PRIOR FILING DATE: 1997-11-24
 ? PRIOR APPLICATION NUMBER: 60/066511
 ? PRIOR FILING DATE: 1997-11-24
 ? PRIOR APPLICATION NUMBER: 60/066770
 ? PRIOR FILING DATE: 1997-11-24
 ? PRIOR APPLICATION NUMBER: 60/069212
 ? PRIOR FILING DATE: 1997-12-11
 ? PRIOR APPLICATION NUMBER: 60/069278
 ? PRIOR FILING DATE: 1997-12-11
 ? PRIOR APPLICATION NUMBER: 60/069334
 ? PRIOR FILING DATE: 1997-12-11
 ? PRIOR APPLICATION NUMBER: 60/069694
 ? PRIOR FILING DATE: 1997-12-16
 ? PRIOR APPLICATION NUMBER: 60/072320
 ? PRIOR FILING DATE: 1998-01-23
 ? PRIOR APPLICATION NUMBER: 60/073612
 ? PRIOR FILING DATE: 1998-02-04
 ? PRIOR APPLICATION NUMBER: 60/074086
 ? PRIOR FILING DATE: 1998-02-09
 ? PRIOR APPLICATION NUMBER: 60/074092
 ? PRIOR FILING DATE: 1998-02-09
 ? PRIOR APPLICATION NUMBER: 60/077791
 ? PRIOR FILING DATE: 1998-03-12
 ? PRIOR APPLICATION NUMBER: 60/078910
 ? PRIOR FILING DATE: 1998-03-20
 ? PRIOR APPLICATION NUMBER: 60/079294
 ? PRIOR FILING DATE: 1998-03-25
 ? PRIOR APPLICATION NUMBER: 60/079663
 ? PRIOR FILING DATE: 1998-02-27
 ? PRIOR APPLICATION NUMBER: 60/079728
 ? PRIOR FILING DATE: 1998-03-27
 ? PRIOR APPLICATION NUMBER: 60/080165
 ? PRIOR FILING DATE: 1998-03-31
 ? PRIOR APPLICATION NUMBER: 60/081203
 ? PRIOR FILING DATE: 1998-04-09
 ? PRIOR APPLICATION NUMBER: 60/081229
 ? PRIOR FILING DATE: 1998-04-09
 ? PRIOR APPLICATION NUMBER: 60/081695
 ? PRIOR FILING DATE: 1998-04-14
 ? PRIOR APPLICATION NUMBER: 60/081817
 ? PRIOR FILING DATE: 1998-04-15
 ? PRIOR APPLICATION NUMBER: 60/081818

? PRIOR FILING DATE: 1998-04-15
 ? PRIOR APPLICATION NUMBER: 60/082999
 ? PRIOR FILING DATE: 1998-04-24
 ? PRIOR APPLICATION NUMBER: 60/083322
 ? PRIOR FILING DATE: 1998-04-28
 ? PRIOR APPLICATION NUMBER: 60/083545
 ? PRIOR FILING DATE: 1998-04-29
 ? PRIOR APPLICATION NUMBER: 60/084600
 ? PRIOR FILING DATE: 1998-05-07
 ? PRIOR APPLICATION NUMBER: 60/084627
 ? PRIOR FILING DATE: 1998-05-07
 ? PRIOR APPLICATION NUMBER: 60/084637
 ? PRIOR FILING DATE: 1998-05-07
 ? PRIOR APPLICATION NUMBER: 60/085149
 ? PRIOR FILING DATE: 1998-05-12
 ? PRIOR APPLICATION NUMBER: 60/085323
 ? PRIOR FILING DATE: 1998-05-13
 ? PRIOR APPLICATION NUMBER: 60/085338
 ? PRIOR FILING DATE: 1998-05-13
 ? PRIOR APPLICATION NUMBER: 60/085339
 ? PRIOR FILING DATE: 1998-05-13
 ? PRIOR APPLICATION NUMBER: 60/085579
 ? PRIOR FILING DATE: 1998-05-15
 ? PRIOR APPLICATION NUMBER: 60/085697
 ? PRIOR FILING DATE: 1998-05-15
 ? PRIOR APPLICATION NUMBER: 60/085704
 ? PRIOR FILING DATE: 1998-05-15
 ? PRIOR APPLICATION NUMBER: 60/086414
 ? PRIOR FILING DATE: 1998-05-22
 ? PRIOR APPLICATION NUMBER: 60/086430
 ? PRIOR FILING DATE: 1998-05-22
 ? PRIOR APPLICATION NUMBER: 60/087106
 ? PRIOR FILING DATE: 1998-05-28
 ? PRIOR APPLICATION NUMBER: 60/088026
 ? PRIOR FILING DATE: 1998-06-04
 ? PRIOR APPLICATION NUMBER: 60/088730
 ? PRIOR FILING DATE: 1998-06-10
 ? PRIOR APPLICATION NUMBER: 60/088741
 ? PRIOR FILING DATE: 1998-06-10
 ? PRIOR APPLICATION NUMBER: 60/088810
 ? PRIOR FILING DATE: 1998-06-10
 ? PRIOR APPLICATION NUMBER: 60/088858
 ? PRIOR FILING DATE: 19/98-06-11
 ? PRIOR APPLICATION NUMBER: 60/089532
 ? PRIOR FILING DATE: 1998-06-17
 ? PRIOR APPLICATION NUMBER: 60/089599
 ? PRIOR FILING DATE: 1998-06-17
 ? PRIOR APPLICATION NUMBER: 60/089907
 ? PRIOR FILING DATE: 1998-06-18
 ? PRIOR APPLICATION NUMBER: 60/089947
 ? PRIOR FILING DATE: 1998-06-19
 ? PRIOR APPLICATION NUMBER: 60/090349
 ? PRIOR FILING DATE: 1998-06-23
 ? PRIOR APPLICATION NUMBER: 60/090429
 ? PRIOR FILING DATE: 1998-06-24
 ? PRIOR APPLICATION NUMBER: 60/090445
 ? PRIOR FILING DATE: 1998-06-24
 ? PRIOR APPLICATION NUMBER: 60/090538
 ? PRIOR FILING DATE: 1998-06-24
 ? PRIOR APPLICATION NUMBER: 60/090863
 ? PRIOR FILING DATE: 1998-06-26
 ? PRIOR APPLICATION NUMBER: 60/091360
 ? PRIOR FILING DATE: 1998-07-01
 ? PRIOR APPLICATION NUMBER: 60/091519
 ? PRIOR FILING DATE: 1998-07-02
 ? PRIOR APPLICATION NUMBER: 60/091982
 ? PRIOR FILING DATE: 1998-07-07

Alignment Scores: 4.89e-30
 Pred. No.: 563.50
 Score: 61.85%
 Percent Similarity: 61.85%
 Best Local Similarity: 44.18%
 Length: 290
 Matches: 110
 Conservative: 44
 Mismatches: 86

```

Query Match:          38.65%      Indels:      9
DB:                   9              Gaps:       4
US-09-598-982-20 (1-771) x US-10-028-072-222 (1-290)

```

```

QY 16 AGAATGTCGGGGGGTCCAGAGGGCCCCAGAGAACAGTGGCCCTGGACGAGTGAAGCTGAGA 75
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 34 ArgmetValGlyGlyGlnAspPrhrngIngluglyGltPrProTprpInValSerIleGln 53
QY 76 GTCACAGCCGCGCTACTGGATGAGCTTTCGGGGGGCTCCCTATCCACCCCGAGTGGGTCG 135
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 54 ArgasnGly-----SerHisPheCysGlyGlySerLeuIleLaGlnIntrPrVal 70
QY 136 CTCACCCCGCCGGCTGGCTGGACCGGCGTCAAGAGATCTGCCCCCGCTCAAGGGGTCAA 195
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 71 LeuThrAlaAlaHisCysPhe---ArgAsnThrSerGluThrSerLeuTyrgInValIleu 89
QY 196 CTGGCGGAGCAACACCTGACTAC-----CAAGACCAAGCTGCTCCGGCTCAAGCAGG 246
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 90 LeuGlyAlaArgGlnIleuValGlnProGlyProHisAlaMetTyrgAlaArgValArgGln 109
QY 247 ATCATGTCACCCCAACAGTGTCTAACACCCCGGCAAGTGGAGCGGACATGCCCTGGAG 306
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 ValGluSerAsnPrroLeuTyrgInglYThraIaSerSerIlaAspValAlaIleuValGlu 129
QY 307 CTGAGAGAGCCGGTGAAGGTCACAGCCCAAGCTGCACACGCTGACACCGCTCCCGCTGCA 366
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 130 LeuGlnAlaProValProPheThrAsnTyrlIleLeuProValCysIleuPrroAspProSer 149
QY 367 GAGACCTTCCCCCGGGAGATGCCCTGGCTGGTCACTGGCTGGGGCGAGTGTGGACAATGAT 426
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 150 ValIlePheGluThrGlyMetIasnCysTrpValThrGlyTrpGlySerProserGluGln 169
QY 427 GAGCCCTCCCAACCGCATTTCTCTGAAAGCAAGTGAAGTCCCATATGAAAAACCCAC 486
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 AspLeuLeuPrroGlnPrroGlyIleLeuGlnLysLeuAlaValProIleIleAspThrPro 189
QY 487 ATTGTGACGCAAAAATACCACCTTGGCGCTACACGGAGACGACGTCCCGCATTCGCTG 546
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 190 LysCysAsnIleuLeuTyrgSerIlyAspPrhrngIlyrPheGlyTyrgIlePrroLysThrIleLys 209
QY 547 GACGACATGCTGTGTGCCGG-----AACACCCGGAGGACACTATGCCAGGCGCACTCC 600
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 210 AsnAspMetIleuCysAlaGlyPheGlnGlnIlyLysIlyAspAlaCysIlySglYAspSer 229
QY 601 GGAGGGCCCTGTGTGSCAAGTGAATGGCACCTGCTGACAGGCGGGCGCTGGTCACTGG 660
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 230 GlyGlyPrroLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaIleValIleSerTrp 249
QY 661 GCGAGGGCTGTGCCCAAGCGCCAGCCCTGGACTTACACCCGCTGCTCACTACTTGG 720
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 250 GlyGlnGlyCysAlaArgGlnAsnArgPrroGlyValTyrlIleArgValAlhrAlaHisHis 269
QY 721 GACTGGATCCACCACTATGTCGCCAAA 747
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 270 AsnTrpIleHisArgIleIleProLys 278

```

```

RESULT 5
US-10-040-655-7
; Sequence 7, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7

```

```

; LENGTH: 290
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-040-655-7

```

```

Alignment Scores:
Pred. No.: 4,89e-30      Length: 290
Score: 563.50          Matches: 110
Percent Similarity: 61.85%      Conservative: 44
Best Local Similarity: 44.18%      Mismatches: 86
Query Match: 38.65%          Indels: 9
DB: 12                  Gaps: 4

```

```

US-09-598-982-20 (1-771) x US-10-040-655-7 (1-290)
QY 16 AGAATGTCGGGGGGTCCAGAGGGCCCCAGAGAACAGTGGCCCTGGACGAGTGAAGCTGAGA 75
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 34 ArgmetValGlyGlyGlnAspPrhrngIngluglyGltPrProTprpInValSerIleGln 53
QY 76 GTCACAGCCGCGCTACTGGATGAGCTTTCGGGGGGCTCCCTATCCACCCCGAGTGGGTCG 135
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 54 ArgasnGly-----SerHisPheCysGlyGlySerLeuIleLaGlnIntrPrVal 70
QY 136 CTCACCCCGCCGGCTGGCTGGACCGGCGTCAAGAGATCTGCCCCCGCTCAAGGGGTCAA 195
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 71 LeuThrAlaAlaHisCysPhe---ArgAsnThrSerGluThrSerLeuTyrgInValIleu 89
QY 196 CTGGCGGAGCAACACCTGACTAC-----CAAGACCAAGCTGCTCCGGCTCAAGCAGG 246
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 90 LeuGlyAlaArgGlnIleuValGlnProGlyProHisAlaMetTyrgAlaArgValArgGln 109
QY 247 ATCATGTCACCCCAACAGTGTCTAACACCCCGGCAAGTGGAGCGGACATGCCCTGGAG 306
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 ValGluSerAsnPrroLeuTyrgInglYThraIaSerSerIlaAspValAlaIleuValGlu 129
QY 307 CTGAGAGAGCCGGTGAAGGTCACAGCCCAAGCTGCACACGCTGACACCGCTCCCGCTGCA 366
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 130 LeuGlnAlaProValProPheThrAsnTyrlIleLeuProValCysIleuPrroAspProSer 149
QY 367 GAGACCTTCCCCCGGGAGATGCCCTGGCTGGTCACTGGCTGGGGCGAGTGTGGACAATGAT 426
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 150 ValIlePheGluThrGlyMetIasnCysTrpValThrGlyTrpGlySerProserGluGln 169
QY 427 GAGCCCTCCCAACCGCATTTCTCTGAAAGCAAGTGAAGTCCCATATGAAAAACCCAC 486
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 AspLeuLeuPrroGlnPrroGlyIleLeuGlnLysLeuAlaValProIleIleAspThrPro 189
QY 487 ATTGTGACGCAAAAATACCACCTTGGCGCTACACGGAGACGACGTCCCGCATTCGCTG 546
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 190 LysCysAsnIleuLeuTyrgSerIlyAspPrhrngIlyrPheGlyTyrgIlePrroLysThrIleLys 209
QY 547 GACGACATGCTGTGTGCCGG-----AACACCCGGAGGACACTATGCCAGGCGCACTCC 600
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 210 AsnAspMetIleuCysAlaGlyPheGlnGlnIlyLysIlyAspAlaCysIlySglYAspSer 229
QY 601 GGAGGGCCCTGTGTGSCAAGTGAATGGCACCTGCTGACAGGCGGGCGCTGGTCACTGG 660
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 230 GlyGlyPrroLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaIleValIleSerTrp 249
QY 661 GCGAGGGCTGTGCCCAAGCGCCAGCCCTGGACTTACACCCGCTGCTCACTACTTGG 720
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 250 GlyGlnGlyCysAlaArgGlnAsnArgPrroGlyValTyrlIleArgValAlhrAlaHisHis 269
QY 721 GACTGGATCCACCACTATGTCGCCAAA 747
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 270 AsnTrpIleHisArgIleIleProLys 278

```

```

RESULT 6
US-10-041-006A-9
; Sequence 9, Application US/10041006A
; Patent No. US20020168754A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia

```

```

; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/041,006A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-041-006A-9

```

```

Alignment Scores:
Pred. No.: 1.9e-29 Length: 315
Score: 554.50 Matches: 109
Percent Similarity: 60.96% Conservative: 44
Best Local Similarity: 43.43% Mismatches: 89
Query Match: 38.03% Indels: 9
DB: Gaps: 4

```

US-09-598-982-20 (1-771) x US-10-041-006A-9 (1-315)

```

OY 10 GAGAAAAGAAATGTCGGGGGTTCAGAGAGCCCGGAGAGCAATGTCGGCCCTGCAGCTGAGC 69
   ::::::::::::::::::::
DB 49 ACPARPLYSILEVALIGLYLTYRALALEUGLUGLUGLUTRPTGTRPRLINVALSER 68
OY 70 CTGAGAGTCCAGCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 129
   ::::::::::::::::::::
DB 69 ILEGIDARGASNGLY-----SERHISRHPCYSGLYGLYSERLEUILEDLAGLUGIN 85
OY 130 TGGGTGCTGACCCGCGCGCGGTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCTCAAG 189
   |||||
DB 86 TRVALLEUETHRALDALAHISCSYRHE--ARGASNTHRSERGLUTHRSERILEUITYRGIN 104
OY 190 GTGCAGACTGCGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
   |||
DB 105 VALLEULEUGLYLADARGIDLEUVALGINPRGIDYRPNHISDALMETLTYRALARGVAL 124
OY 241 AGCAGAGATGATGTCGACCCGCGCGGTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCTCA 300
   ::::::::::::::::::::
DB 125 ARGGLNVALIGLUSERASNPTRGLEUITYRGINLGYTHRALASERSETRALASRYVALDALALEU 144
OY 301 CTGAGAGTCCAGCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
   ::::::::::::::::::::
DB 145 VALGILEUGLADALPROVALPROPHETHIRASNYTYRILEUENPROVALCYSLEUENPROASP 164
OY 361 GCGTCAGAGACTTCCCGCGGGGATGCCGCTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCT 420
   |||
DB 165 PROSERVALILEPHEGLDITHRIGLYMETASNCSYSTRVALTTHRGLYTRPGLYSERPROSER 184
OY 421 AATGTAAAGAGCCGCGCGGTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCTCAATATGGA 480
   ::::::::::::::::::::
DB 185 GIUGLNASRPLEUENPROGLNPRGARGILEUENGINLVSLEADALVALPROLLEILEASP 204
OY 481 AACCCATTTGTGACGCAAAATATACCACTTGGCGCCCTCAAGAGCAGCAGCAGCAGCAGCAGC 540
   |||
DB 205 THRTRPOLYSCYASNLLEUENLEUITYSERILEYASRPHNGILRPHGIDLYTYRGLINPOLYSTR 224
OY 541 GTCGTCGACGACATGCTGTGTCGGGG-----AACCCGAGGAGGAGGATCAATGACGGCC 594
   ::::::::::::::::::::
DB 225 ILEYSASINASPMETLEUCYSALAGLYRHEGLUGLUGLUGLUSYASPRALACYSLSYSGLY 244
OY 595 GACPTCCGGAGGCGCCCTGCTGTGCAAGGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 654
   |||||
DB 245 ASPSERGLYGLYRPLEUENVALCYSLEUENVALGILNSETTRPLEUENLADALVALLE 264
OY 655 AGCTGGGGAGGCGCCGCTGTCACCCAGCCCAACCGCCCTGGCATACACCCGTCACCTTAC 714

```

```

DB 265 SERTRGLYGLUGLYCYSLALARGGLNLSNARGPROGLYVALTYRILEYRVALTHRALA 284
OY 715 TACTTGGAGCTGCAGCCAGCAGCAGTATGCCCAAA 747
DB 285 HISHSASNPTRPLEHNSARGILETRPGLYS 295

```

RESULT 7 US-10-040-655-9

```

; Sequence 9, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-gordon, Patricia
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-040-655-9

```

```

Alignment Scores:
Pred. No.: 1.9e-29 Length: 315
Score: 554.50 Matches: 109
Percent Similarity: 60.96% Conservative: 44
Best Local Similarity: 43.43% Mismatches: 89
Query Match: 38.03% Indels: 9
DB: Gaps: 4

```

US-09-598-982-20 (1-771) x US-10-040-655-9 (1-315)

```

OY 10 GAGAAAAGAAATGTCGGGGGTTCAGAGAGCCCGGAGAGCAATGTCGGCCCTGCAGCTGAGC 69
   ::::::::::::::::::::
DB 49 ACPARPLYSILEVALIGLYLTYRALALEUGLUGLUGLUTRPTGTRPRLINVALSER 68
OY 70 CTGAGAGTCCAGCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 129
   ::::::::::::::::::::
DB 69 ILEGIDARGASNGLY-----SERHISRHPCYSGLYGLYSERLEUILEDLAGLUGIN 85
OY 130 TGGGTGCTGACCCGCGCGCGGTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCTCAAG 189
   |||||
DB 86 TRVALLEUETHRALDALAHISCSYRHE--ARGASNTHRSERGLUTHRSERILEUITYRGIN 104
OY 190 GTGCAGACTGCGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
   |||
DB 105 VALLEULEUGLYLADARGIDLEUVALGINPRGIDYRPNHISDALMETLTYRALARGVAL 124
OY 241 AGCAGAGATGATGTCGACCCGCGCGGTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCTCA 300
   ::::::::::::::::::::
DB 125 ARGGLNVALIGLUSERASNPTRGLEUITYRGINLGYTHRALASERSETRALASRYVALDALALEU 144
OY 301 CTGAGAGTCCAGCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
   ::::::::::::::::::::
DB 145 VALGILEUGLADALPROVALPROPHETHIRASNYTYRILEUENPROVALCYSLEUENPROASP 164
OY 361 GCGTCAGAGACTTCCCGCGGGGATGCCGCTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCT 420
   |||
DB 165 PROSERVALILEPHEGLDITHRIGLYMETASNCSYSTRVALTTHRGLYTRPGLYSERPROSER 184
OY 421 AATGTAAAGAGCCGCGCGGTGCGTGGGGAGCCGATCAAGATCTGGCCCGCCCTCAATATGGA 480
   ::::::::::::::::::::
DB 185 GIUGLNASRPLEUENPROGLNPRGARGILEUENGINLVSLEADALVALPROLLEILEASP 204

```

```

QY 481 AACCAATTTGTGACGCCAATAAATACCACTTTGGCGCTACAGCGGAGAGCAAGCTCCGCATC 540
DB 205 ThrProLysCysAsnLeuLeuLeuTyrSerLysAspThrGlnPheGlnYTrGlnProLysThr 224
QY 541 GTCCTGGAGCAATGCTGTGTGCTCCGGG-----AACACCCGGAGGACATCAATGCCAGGGC 594
DB 225 ILeLysAsnAspMetLeuLysAlaGlyPheGlnGlnGlyLysLysAspAlaCysLysGly 244
QY 595 GACTCCGGAGGGCCCTGTGTGTGCAAGGTGAATGGCACCTGGCTGCAGCGGGCGGTGC 654
DB 245 AspSerGlyGlyProLeuValCysLeuValGlyGlnSerThrLeuGlnIlaGlyValIle 264
QY 655 ACCTGGGGGAGGGCTGTGTGCCCAAGCCCAACCGGCTGCATGTACACCCGTGTACCTTAC 714
DB 265 SerTrpGlyGlnGlyCysAlaIleAsnArgGlnAsnArgProGlyValIleYTrIleArgValThrAla 284
QY 715 TACTTGGACTGGATCCACCACTAATGCCCGCAAA 747
DB 285 HISHLSAsnTrpIleHisArgIleIleProLys 295

```

```

RESULT 8
US-10-041-400A-7
: Sequence 7, Application US/10041400A
: Patent No. US20020110895A1
: GENERAL INFORMATION:
: APPLICANT: Darrow, Andrew
: APPLICANT: Andrade-Gordon, Patricia
: APPLICANT: Qi, Jenson
: TITLE OF INVENTION: DNA Encoding the Human Serine
: FILE REFERENCE: ORT-1031
: CURRENT APPLICATION NUMBER: US/10/041,400A
: PRIOR FILING DATE: 2002-01-08
: PRIOR APPLICATION NUMBER: US/09/387,375
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 284
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-041-400A-7

```

```

Alignment Scores:
Pred. No.: 2,866-28
Score: 536.50
Percent Similarity: 58.54%
Best Local Similarity: 45.53%
Query Match: 36.80%
DB: 12 Gaps: 4
US-09-598-982-20 (1-771) x US-10-041-400A-7 (1-284)

```

```

QY 7 CTCGAGAAAGAAATGCTGGGGGTGACGAGAGCCCGGAGGCAAGTGGCCCTGGCAGGTG 66
DB 33 MetSerSerArgIleValAlaGlyIleArgAspGlyArgAspGlyGlnIleProIleGlnIla 52
QY 67 AGCTGAGAGTCCAGCGCCCATATACATGACATCTTGTGGGGGCTCCCTCATCCAGCC 126
DB 53 SerIleGlnHisProGly-----AlaHisValCysGlyGlySerLeuIleAlaPro 69
QY 127 CAGTGGGTGCTGACCGCGCCGCTGCGGACCGGACGTCAAGGATGCTGGCGCCGCTC 186
DB 70 GlnTrpValLeuThrAlaIleHisCysPhe---ProArgArgAlaLeuProIlaGlnIleYTr 88
QY 187 AGGTGCAACTGTCGGGAGGAGCACTC-----TACTACAGGAGCAAGCTGCTGGCCG 237
DB 89 ArgValIleArgLeuGlyValAlaLeuArgLeuGlySerThrSerProArgIleGlnIleValPro 108
QY 238 GTCAGAGAGATGATGCTGACCCCAAGTTCATACCGCCCAAGATGGAGGAGGAGCAATCGCC 297
DB 109 ValArgArgValLeuLeuLeuProAspIleYTrSerGlnAspGlyAlaIleArgGlyLysPheAla 128

```

```

QY 298 CTCGTGAGACCTGGAGAGCCGGTGAAGTCTCCAGCCAGCTCCAGCAAGCTCACCTGGCC 357
DB 129 LeuLeuGlnIleuArgArgProValIProLeuSerAlaArgValGlnProValCysLysLeu 148
QY 358 CCTGCCCTCAAGAACCTTCCCGCGGAGATGCCGTGTGGGTACATGCTGGGGCCATGTCG 417
DB 149 ValProGlyAlaArgProProProGlyThrProCysArgValThrGlyIlePheGlySerLeu 168
QY 418 GACAAATGATGAGCGCCCTCCCGCAATTTGCTGAAAGCAGCAGGACAGGATGCCCAATATG 477
DB 169 ArgProGlyValIProLeuProGlnIleTrpArgProLeuGlnIleValIleArgValIProLeuLys 188
QY 478 GAACAACCAATTTGTGACGCCAATAAATACCACTTTGGCGCTACAGCGGAGAGCAAGCTCCGC 537
DB 189 AspSerArgThrCysAspIleLeuLeuYTrHisValGlyAlaAspValIProGlnIlaGlnArg 208
QY 538 ATCTGCTGGTGCAGACATGCTGTGTGCTCCGGG-----AACACCCGGAGGACATCAATGCCAG 591
DB 209 ILeValLeuProGlySerLeuLysAlaGlyYTrProGlnGlyHisLysAspAlaCysGln 228
QY 592 GCGGACTCCGGAGGGCCCTGTGTGTGCAAGGTGAATGGCACCTGGCTGCAGCGGGCGGTGC 651
DB 229 GlnAspSerGlyGlyProLeuThrCysLeuGlnSerIleYTrValIleValIleValI 248
QY 652 CTCAGCTGGGGGAGGGCTGTGTGCCCAAGCCCAACCGGCTGCATGTACACCCGTGTACCC 711
DB 249 ValSerTrpGlyLysGlyCysAlaIleuProAsnArgProGlyValIleYTrIleSerValAla 268
QY 712 TACTTGGACTGGATCCACCACTAATGCCCGCAAA 747
DB 269 ThrYTrSerProIle 274

```

```

RESULT 9
US-10-041-264A-7
: Sequence 7, Application US/10041264A
: Patent No. US20020142446A1
: GENERAL INFORMATION:
: APPLICANT: Darrow, Andrew
: APPLICANT: Andrade-Gordon, Patricia
: APPLICANT: Qi, Jenson
: TITLE OF INVENTION: DNA Encoding the Human Serine
: FILE REFERENCE: ORT-1031
: CURRENT APPLICATION NUMBER: US/10/041,264A
: PRIOR FILING DATE: 2002-01-08
: PRIOR APPLICATION NUMBER: US/09/387,375
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 284
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-041-264A-7

```

```

Alignment Scores:
Pred. No.: 2,866-28
Score: 536.50
Percent Similarity: 58.54%
Best Local Similarity: 45.53%
Query Match: 36.80%
DB: 12 Gaps: 4
US-09-598-982-20 (1-771) x US-10-041-264A-7 (1-284)

```

```

QY 7 CTCGAGAAAGAAATGCTGGGGGTGACGAGAGCCCGGAGGCAAGTGGCCCTGGCAGGTG 66
DB 33 MetSerSerArgIleValAlaGlyIleArgAspGlyArgAspGlyGlnIleProIleGlnIla 52
QY 67 AGCTGAGAGTCCAGCGCCCATATACATGACATCTTGTGGGGGCTCCCTCATCCAGCC 126
DB 53 SerIleGlnHisProGly-----AlaHisValCysGlyGlySerLeuIleAlaPro 69

```

```

OY 127 CAGTGGTGTGTGACCCCGCGGCTGCGGGGAGCCGTCACAGGATCTGCGCCCTC 186
DB 70 GlnTrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTrp 88
OY 187 AGGTGCAACCTGGGAGCAGCAGCCTC-----TACTACAGGAGCCAGCTGCGCC 237
DB 89 ArgValAlaGluLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValPro 108
OY 238 GTCACAGGATGATGTCACCCACAGTTCACACCGCCCAAGTCAGGAGCCAGCAATGCGC 297
DB 109 ValAlaGluValLeuLeuProProAspPylrSerGluAspGlyAlaArgGlyAspLeuAla 128
OY 288 CTGTGTGAGCTGTGAGAGCCGCTGAGGCTGTCCAGCCAGCTCCAGCCAGCTCCAGCTCC 357
DB 129 LeuLeuGlnLeuAlaArgArgProValAlaProLeuSerAlaArgValGlnProValCysLeuPro 148
OY 358 CCTGCTCAGAGACCTTCCCGCGGGGATGCGGTGCTGGGTACTGTGGTGGGCGATGTG 417
DB 149 ValProGlyAlaArgProProProGlyThrProCysAlaGlyAlaThrGlyTrpGlySerLeu 168
OY 418 GACAAATGATGAGCCGCTCCACAGTTCCTGTGAAAGCAGGTGAAAGTCCCAATGATG 477
DB 169 ArgProGlyValProLeuProGluTrpArgProLeuGlnGlyValAlaArgValProLeuLeu 188
OY 478 GAAACACACATTTGTGACGCAAAATACACCTTGGCGCCCTACACGCGAGACAGCTCCGC 537
DB 189 AspSerArgThrCysAspArgLeuThrHisValGlyAlaAspValProGlnAlaGluArg 208
OY 538 ATGCTCCGTGACGACATGCTGTGTGCGCGGG-----AACACCCGGAGGAGTCAATGCCAG 591
DB 209 IleValLeuProGlySerLeuCysAlaGlyTrpProGlnGlnHisIleAspAlaCysGln 228
OY 592 GGCAGCTCCGGAGGCGCCCTGTGTGCAAGGTGAAATGAGCAGCTGGCTGAGCGCGCGT 651
DB 228 GlyAspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyVal 248
OY 652 GTCACCTGGGCGGAGGCTGTGTGCCAGCCCAACCGGCTGAGCTACACCCGCTGACCC 711
DB 249 ValSerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValIleTrpSerValAla 268
OY 712 TACTACTTGGACTGGATC 729
DB 269 ThrTyrSerProTrpIle 274

RESULT 10
US-10-042-091A-7
; Sequence 7, Application US/10042091A
; Patent No. US20020142447A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Qi, Jenson
; TITLE OF INVENTION: DNA Encoding the Human Serine
; TITLE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/10/042, 091A
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US/09/387, 375
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-091A-7

Alignment Scores: 2.86e-28 Length: 284
Pred. No.: 536.50 Matches: 112
Score: 58.548 Conservative: 32
Percent Similarity: 45.538 Mismatches: 93
Best Local Similarity: 36.80% Indels: 9
Query Match:

```

```

DB: 12 Gaps: 4
US-09-598-982-20 (1-771) x US-10-042-091A-7 (1-284)
OY 7 CTCGAGAAAGATGCTGGGGGTCAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTG 66
DB 33 MetSerSerArgIleValGlyIleArgAspGlyArgAspGlyGluTrpProTrpIleAla 52
OY 67 AGCCGAGAGTCCACGGCCCAATGACATGACATGCACTTCCTGGGGGCTCCATCCAGCC 126
DB 53 SerIleGlnHisProGly-----AlaHisValCysGlyGlySerLeuLeuAlaPro 69
OY 127 CAGTGGTGTGTGACCCCGCGGCTGCGGGGAGCCGTCACAGGATCTGCGCCCTC 186
DB 70 GlnTrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTrp 88
OY 187 AGGTGCAACCTGGGAGCAGCAGCCTC-----TACTACAGGAGCCAGCTGCGCC 237
DB 89 ArgValAlaGluLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValPro 108
OY 238 GTCACAGGATGATGTCACCCACAGTTCACACCGCCCAAGTCAGGAGCCAGCAATGCGC 297
DB 109 ValAlaGluValLeuLeuProProAspPylrSerGluAspGlyAlaArgGlyAspLeuAla 128
OY 288 CTGTGTGAGCTGTGAGAGCCGCTGAGGCTGTCCAGCCAGCTCCAGCCAGCTCCAGCTCC 357
DB 129 LeuLeuGlnLeuAlaArgArgProValAlaProLeuSerAlaArgValGlnProValCysLeuPro 148
OY 358 CCTGCTCAGAGACCTTCCCGCGGGGATGCGGTGCTGGGTACTGTGGTGGGCGATGTG 417
DB 149 ValProGlyAlaArgProProProGlyThrProCysAlaGlyAlaThrGlyTrpGlySerLeu 168
OY 418 GACAAATGATGAGCCGCTCCACAGTTCCTGTGAAAGCAGGTGAAAGTCCCAATGATG 477
DB 169 ArgProGlyValProLeuProGluTrpArgProLeuGlnGlyValAlaArgValProLeuLeu 188
OY 478 GAAACACACATTTGTGACGCAAAATACACCTTGGCGCCCTACACGCGAGACAGCTCCGC 537
DB 189 AspSerArgThrCysAspArgLeuThrHisValGlyAlaAspValProGlnAlaGluArg 208
OY 538 ATGCTCCGTGACGACATGCTGTGTGCGCGGG-----AACACCCGGAGGAGTCAATGCCAG 591
DB 209 IleValLeuProGlySerLeuCysAlaGlyTrpProGlnGlnHisIleAspAlaCysGln 228
OY 592 GGCAGCTCCGGAGGCGCCCTGTGTGCAAGGTGAAATGAGCAGCTGGCTGAGCGCGCGT 651
DB 228 GlyAspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyVal 248
OY 652 GTCACCTGGGCGGAGGCTGTGTGCCAGCCCAACCGGCTGAGCTACACCCGCTGACCC 711
DB 249 ValSerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValIleTrpSerValAla 268
OY 712 TACTACTTGGACTGGATC 729
DB 269 ThrTyrSerProTrpIle 274

RESULT 11
US-10-041-400A-9
; Sequence 9, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Qi, Jenson
; TITLE OF INVENTION: DNA Encoding the Human Serine
; TITLE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/10/041, 400A
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US/09/387, 375
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0

```



```

: SEQ ID NO 9
: LENGTH: 316
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Amino acid
: OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-9

```

Alignment Scores:

```

Pred. No.: 1.11e-27 Length: 316
Score: 527.50 Matches: 111
Percent Similarity: 57.96% Conservative: 31
Best Local Similarity: 45.31% Mismatches: 94
Query Match: 36.18% Indels: 9
DB: 12 Gaps: 4

```

US-09-598-982-20 (1-771) x US-10-041-400A-9 (1-316)

```

OY 10 GAGAAAGAAATGTCGGGGGTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGC 69
   ::::::::::::::::::::
Db 49 ASPAARPLYSILEVALGILYGLYTRALALEUGLUAASRGLIUTRPRTRPRLMALASER 68
OY 70 CTGAGAGTCCACGGCCCACTGATGCACTTCTGGGGGGCTCCATCCACCCCGAG 129
   ::::::::::::::::::::-LANHSVALGYSGLYGLYSERLEUILELABRGLIN 85
Db 69 ILEGLNHSRPROGLY-----LANHSVALGYSGLYGLYSERLEUILELABRGLIN 85
OY 130 TGGGTGTCAGACCCCGGGCGCTGGTGGACCGGACGTCAGAGATGTCGCCCTCCAGG 189
   ::::::::::::::::::::
Db 86 TRVALLEUPTHALALAHISCSYPHE---PROARGATGALALEURPROVALAGLUTRYARG 104
OY 190 GTCSAAGTGGCGGAGCAGCAGCTC-----TACTACCAAGAGCAGAGCTGGCCGGGTC 240
   ::::::::::::::::::::
Db 105 VALARGLEUGLALALEUARGLEUGLISERTHRSERPROARGLTHLEUSERVALPROVAL 124
OY 241 AGCAGGATTCATGTCACCCACAGCTTACACCGCCCGGACATCGAGACATCCGCCCTG 300
   ::::::::::::::::::::
Db 125 ARGATGVALLEUURPROKSPRYRSEGLUAASRGLIUALAARGLYASRLEUALALEU 144
OY 301 CTGAGAGTCCACGGCCCACTGATGCACTTCTGGGGGGCTCCATCCACCCCGAG 129
   ::::::::::::::::::::
Db 145 LEUGLNLLEUARGYRPROVALPROLEUSERGALAAARGVALGILNPROVALCYSLEURPROVA 164
OY 361 GCCATGAGACACTTCCCGCGGGGATGCGGTCGTCGTCAGTGGCTGGGGCGATGAGAC 420
   ::::::::::::::::::::
Db 165 PROGLYALALARGPROBROGLYTHRPROCSARGVALTHGLYTRPGLYSERLEUARG 184
OY 421 AATGATGAGCCCTCCACCGCCATTTCTGAAAGSAGSAGTGAAGTCCCAATTAATGGA 480
   ::::::::::::::::::::
Db 185 PROGLYVALPROLEURPROGLIUTRPRARGPROLEUGLNGLYVALAARGVALPROLEUASP 204
OY 481 AACCAATTTGTGAGGCAAAATACCACTTGGCCCTGACAGCGGAGACAGCAGCTCCGATC 540
   ::::::::::::::::::::
Db 205 SERATGTLHCYSASRGLYLEUURTHISVALGILUALAASRVALPROGLNALAGLUTRYGLE 224
OY 541 GTCGCTGAGACACTTCTGTCGCCGG-----AACACCCGGGAGGACTCATGCCAGGC 594
   ::::::::::::::::::::
Db 225 VALLEURPROGLYSERLEUCYSALAGLYTRPROGLNGLYHLSLVSARALAEYSGLNGLY 244
OY 595 GACTCCGGAGGGCCCTGGTGTGCAAGGTAATGSCACCTGGCTCCAGGCGGGCGTGTGTC 654
   ::::::::::::::::::::
Db 245 ASPSERGLYGLYRPROLEUPTHRCYSLEUGLNSERGLYSERTRVALLEUVALGILYVALA 264
OY 655 AGCTGGGGGAGGGGCTGTCAGGCAAAACCGCCCTGAGATTAACACCCGTCACATPAC 714
   ::::::::::::::::::::
Db 265 SERTTRPGLYLSGLYCYSALALEURPROASNDARGPROGLYVALYTHRSHERVALADATHR 284
OY 715 TACTTGGACTGGATC 729
   ::::::::::::::::::::
Db 285 TYRSESRPROTRPILIE 289

```

```

RESULT 12
US-10-041-264A-9

```

```

: Sequence 9, Application US/10041264A
: Patent No.: US20020142446A1
: GENERAL INFORMATION:
: APPLICANT: Dartow, Andrew
: APPLICANT: Andrade-Gordon, Patricia
: APPLICANT: Qi, Jenson
: TITLE OF INVENTION: DNA Encoding the Human Serine
: TITLE OF INVENTION: Pro tease EOS
: FILE REFERENCE: ORT-1031
: CURRENT APPLICATION NUMBER: US/10/041,264A
: CURRENT FILING DATE: 2002-01-08
: PRIOR APPLICATION NUMBER: 05/09/387,375
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patentl Ver. 2.0
: SEQ ID NO 9
: LENGTH: 316
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Amino acid
: OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-264A-9

```

Alignment Scores:

```

Pred. No.: 1.11e-27 Length: 316
Score: 527.50 Matches: 111
Percent Similarity: 57.96% Conservative: 31
Best Local Similarity: 45.31% Mismatches: 94
Query Match: 36.18% Indels: 9
DB: 12 Gaps: 4

```

US-09-598-982-20 (1-771) x US-10-041-264A-9 (1-316)

```

OY 10 GAGAAAGAAATGTCGGGGGTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGC 69
   ::::::::::::::::::::
Db 49 ASPAARPLYSILEVALGILYGLYTRALALEUGLUAASRGLIUTRPRTRPRLMALASER 68
OY 70 CTGAGAGTCCACGGCCCACTGATGCACTTCTGGGGGGCTCCATCCACCCCGAG 129
   ::::::::::::::::::::-LANHSVALGYSGLYGLYSERLEUILELABRGLIN 85
Db 69 ILEGLNHSRPROGLY-----LANHSVALGYSGLYGLYSERLEUILELABRGLIN 85
OY 130 TGGGTGTCAGACCCCGGGCGCTGGTGGACCGGACGTCAGAGATGTCGCCCTCCAGG 189
   ::::::::::::::::::::
Db 86 TRVALLEUPTHALALAHISCSYPHE---PROARGATGALALEURPROVALAGLUTRYARG 104
OY 190 GTCSAAGTGGCGGAGCAGCAGCTC-----TACTACCAAGAGCAGAGCTGGCCGGGTC 240
   ::::::::::::::::::::
Db 165 PROGLYALALARGPROBROGLYTHRPROCSARGVALTHGLYTRPGLYSERLEUARG 184
OY 190 GTCSAAGTGGCGGAGCAGCAGCTC-----TACTACCAAGAGCAGAGCTGGCCGGGTC 240
   ::::::::::::::::::::
Db 105 VALARGLEUGLALALEUARGLEUGLISERTHRSERPROARGLTHLEUSERVALPROVAL 124
OY 241 AGCAGGATTCATGTCACCCACAGCTTACACCGCCCGGACATCGAGACATCCGCCCTG 300
   ::::::::::::::::::::
Db 125 ARGATGVALLEUURPROKSPRYRSEGLUAASRGLIUALAARGLYASRLEUALALEU 144
OY 301 CTGAGAGTCCACGGCCCACTGATGCACTTCTGGGGGGCTCCATCCACCCCGAG 129
   ::::::::::::::::::::
Db 145 LEUGLNLLEUARGYRPROVALPROLEUSERGALAAARGVALGILNPROVALCYSLEURPROVA 164
OY 361 GCCATGAGACACTTCCCGCGGGGATGCGGTCGTCGTCAGTGGCTGGGGCGATGAGAC 420
   ::::::::::::::::::::
Db 165 PROGLYALALARGPROBROGLYTHRPROCSARGVALTHGLYTRPGLYSERLEUARG 184
OY 421 AATGATGAGCCCTCCACCGCCATTTCTGAAAGSAGSAGTGAAGTCCCAATTAATGGA 480
   ::::::::::::::::::::
Db 185 PROGLYVALPROLEURPROGLIUTRPRARGPROLEUGLNGLYVALAARGVALPROLEUASP 204
OY 481 AACCAATTTGTGAGGCAAAATACCACTTGGCCCTGACAGCGGAGACAGCAGCTCCGATC 540
   ::::::::::::::::::::
Db 205 SERTTRPGLYLSGLYCYSALALEURPROASNDARGPROGLYVALYTHRSHERVALADATHR 224
OY 541 GTCGCTGAGACACTTCTGTCGCCGG-----AACACCCGGGAGGACTCATGCCAGGC 594
   ::::::::::::::::::::
Db 225 VALLEURPROGLYSERLEUCYSALAGLYTRPROGLNGLYHLSLVSARALAEYSGLNGLY 244

```



```

OY 241 AGCAGGATCATGCTGACACCACAGCTTCTACACCCGCCAGATGCGAGCGGACATGCGCTG
    ||||| ||||| :||| :||| ||||| |||||
DB 118 LysAspRIleIleProHisProSerTyrIleuGlnGluYserGlnGlyAspRIleAlaIeu 137
OY 301 CTGAGCTGAGGAGGAGCCGGTGAAGGTCTCCAGCCAGCTCCAGCCAGCTCCAGCTCCGCT
    ||||| ||||| :||| :||| ||||| |||||
DB 138 LeuGlnLeuSerArgProIleThrPheSerArgTyrIleArgProIleCysLeuProAla 157
OY 361 GCGTGAAGACCTTCCCGCGGGGATGCCGTGGTACGTACGTGGTGGGCGCATGTGGAC 420
    ||||| :||| ||||| ||||| :||| ||||| ||||| |||||
DB 158 AlaAsnAlaSerPheProAsnGlyLeuHisCysThrValThrGlyTyrPclHisValAla 177
OY 421 AATGATGAGCGCTCCAGCCGATTTCTGAAAGAGTGAAGGTGCCCAATATGGA 480
    ||| ||| ||| ||||| :||| ||||| :||| |||||
DB 178 ProSerValSerLeuLeuThrProLysProLeuGlnGlnIleValProLeuIleSer 197
OY 481 AACCAATTTGTAGCCCAAAATACCACTTGGCGCTACACGGGAGAGCCAGCTCCGCATC 540
    ||| :||| :||| :||| :||| :||| :||| :|||
DB 198 ArgGluThrCysAsnCysLeuTyrAsnIleAspAla---LysProGluGluProHisPhe 216
OY 541 GTCCTGAGCAATATGCTGTGTGTCGGCGGAAACACCCGG-----AGGACTCATGCCAGGCG 594
    ||| :||| :||| :||| :||| :||| :||| :|||
DB 217 ValGlnGluAspMetValCysAlaGlyTyrValGlnGlyGlyLysAspAlaCysGlnGly 236
OY 595 GACTCCGGAGGCGCCCTGCTGTCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGGTGC 654
    ||||| ||||| ||||| ||| ||| ||| ||||| :|||
DB 237 AspSerGlyGlyProLeuSerCysProValGlnGlyLeuTyrTyrLeuThrGlyIleVal 256
OY 655 ACCTGGGGGAGGCGGTGTGCCAGCCCAACCGGCTGCATCTACACCCGCTGCACCTAC 714
    ||||| ||||| :||| :||| :||| :||| :||| :|||
DB 257 SerTyrGlyAspAlaCysGlyIleArgAsnArgProGlyValTyrThrIleuAlaSerSer 276
OY 715 TACTTGGACTGGATCCACCATATGTC 741
    ||| ||||| |||||
DB 277 TyrAlaSerTyrIleGlnSerLysVal 285
    ||| ||||| |||||
RESULT 15
US-10-067-761-19
: Sequence 19, Application US/10067761
: Publication No. US20020197701A1
: GENERAL INFORMATION:
: APPLICANT: Shi et al.
: TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
: FILE REFERENCE: PT005P4
: CURRENT APPLICATION NUMBER: US/10/067,761
: PRIORITY FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: 09/804,156
: PRIOR FILING DATE: 2001-03-13
: PRIOR APPLICATION NUMBER: 60/189,025
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 19
: LENGTH: 238
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-067-761-19

```

```

Alignment Scores:
Pred. No.: 3,53e-26 Length: 238
Score: 504.50 Matches: 106
Percent Similarity: 59.73% ConservatIve: 26
Best Local Similarity: 47.96% Mismatches: 76
Query Match: 34.60% Indels: 13
DB: 9 Gaps: 6
US-09-598-982-20 (1-771) x us-10-067-761-19 (1-238)

```

```

OY 16 AGAATGCTGGGGGCTGAGGAGGCGCCCGCAGAGCAATGCTGGCGAGGCTGAGCTGAGA 75
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 29 ArgIleValGlyGlyHisAlaIleProAlaGlyAlaIleTyrProIleAlaSerLeuArg 48

```

```

OY 76 GTCCACGGCCCAATCTGATGCACTTCTGCGGGGCTCCCTCATCCACCCAGCTGGGTG 135
    :||| :||| ||||| ||||| ||||| |||||
DB 49 LeuArgArg-----ValHisValCysGlyGlySerLeuLeuSerProGlnIleVal 65
OY 136 CTGACCCCGCCGGCGTGCCTGGGAGCCGGAGCTCAAGATCTGGCCGCTCAGGGTGA 195
    ||||| ||||| ||||| ||||| ||||| |||||
DB 66 LeuThrAlaIleHisCysPheSerGlySerLeuAsnSer---SerAspTyrGlnValHis 84
OY 196 CTGGCGGAGACACACCTCTGACTACAGAGACAGCTGCTCCCGGTGAGCAATCATCTG 255
    ||| ||| :||| :||| ||||| ||||| :|||
DB 85 LeuGlyGlyLeuGlnIleThrLeuSerProHisPheSerThrValArgGlnIleIleu 104
OY 256 CACCCAACTCTTACACCGCCAGATCGGA-----GCGACATGCGCCCTGCTGGAGCTG 309
    ||| ||| :||| ||| ||| ||||| ||||| |||||
DB 105 HisSerSer---ProSerGlyGlnProGlyThrSerGlyAspRIleAlaIleuValGluIeu 123
OY 310 GAGGAGCCGGTGAAGGTCTCCAGCCAGCTCCACACGCTCCAGCCCTGCCCTCCAGAG 369
    ||||| :||| :||| :||| :||| :||| :|||
DB 124 SerValProValThrLeuSerSerArgIleLeuProValCysLeuProGluAlaSerAsp 143
OY 370 ACCTTCCCGCCGGGATGCCGTGGTCACTGGCTGGGCGGATGTGGACAATGATGAG 429
    ||| ||||| :||| :||| ||||| ||||| |||||
DB 144 AspPheCysProGlyIleArgCysTyrValThrGlyTyrGlyTyrThrArgGlnGlyIu 163
OY 430 CGCTCCCAACCCCAATTTCTCTGAAAGCAGTGAAGGTGCCCATATGGAATAACCAAT 489
    ||||| ||||| ||||| :||| :||| :||| :|||
DB 164 ProLeuProProProTyrSerLeuArgGluValLysValSerValValAspThrGluThr 183
OY 490 TGTGACGCCAAAATACCACTTGGCGCTTACACGGGAGAGACGCTCCGCTGCTGTCAC 549
    ||| ||| :||| ||| ||| ||||| |||||
DB 184 CysArgArgAsp-----TyrProGlyProGlyGlySerIleLeuGlnPro 198
OY 550 GACTTCTGTGTGCGCGGAAACACCCGGAGGACTATGCCAGGGGAGCTCCGAGAGGCC 609
    ||||| ||||| ||||| ||||| ||||| |||||
DB 199 AspMetLeuCysAlaIleArgGlyPro---GlyAspAlaCysGlnAspSerGlyGlyPro 217
OY 610 CTGCTGTGCAAGGTGAATGAGCACTGGCTGCAGGCGGGCGGTGCAGCTGGGCGGAGGCG 669
    ||||| ||||| :||| ||||| ||||| ||||| |||||
DB 218 LeuValCysGlnValAsnGlyAlaIleThrValGlnAlaGlyThrValSerTyrPclGlyGly 237
OY 670 TGT 672
    |||
DB 238 Cys 238

```

Search completed: January 31, 2003, 07:16:39
Job time : 45 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - protein search, using frimem_n2p model

Run on: January 31, 2003, 06:51:34 ; Search time 25.5 Seconds

(without alignments)
\$B13.305 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 1458

Sequence: 1 gggcccccgcgagaagaat.....cgtgaagcggccgcgcgtrcgt 771

Scoring table: BIOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frimem_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO/spool/US09598982/unat_27012003_073717_19581/app_query.fasta.1.967
-DB=PIR.73 -QEMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=3000000000
-USER=US09598982.@CN.L1.15.@unat_27012003_073717_19581 -NCPU=6 -ICPU=3
-NO_XLPRXY -NO_MMAP -LARGEQUERY -NEB_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: PIR.73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB ID	Description
1	1368	93.8	275	2	B35863
2	1363	93.5	275	2	A35863
3	1339	91.8	275	2	C35863
4	1232.5	84.5	274	2	A45754
5	1092	74.9	276	2	A38654
6	1077	73.9	275	2	A32410
7	1075	73.7	270	2	S56160
8	1057	72.5	273	2	A47246
9	1055	72.4	274	2	JC41171
10	1005	68.9	237	2	S68702
11	808	55.4	230	2	I48685
12	684.5	46.9	269	2	B32410
13	512	35.1	343	1	A57014
14	467	32.0	625	1	KFH01

15	451	30.9	638	1	KOHUP	Plasma kallikrein
16	448	30.7	455	2	A61545	Plasma (EC 3.4.21
17	447	30.7	638	1	KOMSPL	Plasma kallikrein
18	446.5	30.6	812	1	PLBO	Plasmin (EC 3.4.21
19	445	30.5	638	1	KORPL	Plasma kallikrein
20	444.5	30.5	271	1	ELRRT2	pancreatic elastas
21	443	30.4	245	1	KYBOB	chymotrypsin (EC 3
22	441	30.2	460	2	B61545	Plasmin (EC 3.4.21
23	439.5	30.1	269	2	B26823	pancreatic elastas
24	437	30.0	1524	2	T30337	polyprotein - Atri
25	430.5	29.5	271	2	A25528	pancreatic elastas
26	429	29.4	810	1	PLHU	Plasma (EC 3.4.21
27	428	29.4	263	2	A21195	Plasmin (EC 3.4.21
28	427	29.3	263	2	B30848	Plasmin (EC 3.4.21
29	427	29.3	266	1	ERPG	pancreatic elastas
30	426	29.2	263	2	A31299	chymotrypsin (EC 3
31	422	28.9	263	1	KYRTB	chymotrypsin (EC 3
32	420.5	28.8	812	1	PLMS	Plasmin (EC 3.4.21
33	420	28.8	786	1	A47547	serine proteinase
34	419	28.7	245	1	KYBOA	chymotrypsin (EC 3
35	419	28.7	558	2	UC5878	Plasma hyaluronan-
36	419	28.7	790	1	PLPG	Plasmin (EC 3.4.21
37	416.5	28.6	246	2	B25528	trypsin (EC 3.4.21
38	414.5	28.4	246	1	TRRT2	trypsin (EC 3.4.21
39	414.5	28.4	264	2	I38136	chymotrypsin-like
40	413.5	28.4	269	2	C26823	pancreatic elastas
41	413.5	28.4	367	2	JF0104	testicular serine
42	412.5	28.3	246	1	TRRT1	trypsin (EC 3.4.21
43	412	28.3	267	2	S70439	pancreatic elastas
44	412	28.3	257	4	A56615	probable pancreati
45	411	28.2	1420	2	A32869	apolipoprotein(a)

ALIGNMENTS

RESULT 1
B35863
trypase (EC 3.4.21.59) II precursor - human
N:Alternate names: trypase beta
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: B35863; A37193; I59473
R:VanderSlide, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A:Title: Human mast cell trypase: multiple cDNAs and genes reveal a multigene serine
A:Reference number: A35863; MUID:90251647; PMID:2187193
A:Accession: B35863
A:Molecule type: mRNA; DNA
A:Residues: 1-275 <VAN>
A:Cross-references: GB:M33492; NID:q3339982; PIDN:AAA36779.1; PID:q3339983
A>Note: residues 2-275 are derived from mRNA; residue one was inferred from the genom
R:Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A:Title: Cloning and characterization of a second complementary DNA for human tryptas
A:Reference number: A37193; MUID:90369005; PMID:2203827
A:Accession: A37193
A:Molecule type: mRNA
A:Residues: 1-275 <MII>
A:Cross-references: GB:M37488; NID:q179583; PIDN:AAA51843.1; PID:q179584
R:Blom, T.; Hellman, L.
Scand. J. Immunol. 37, 203-208, 1993
A:Title: Characterization of a trypase mRNA expressed in the human basophil cell 11n
A:Reference number: I59473; MUID:93166209; PMID:8434231
A:Accession: I59473
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-275 <RES>
A:Cross-references: GB:S55551; NID:q265666; PIDN:AAD13876.1; PID:q4261576
A:Experimental source: basophil cell line KUB12
C:Genetics:
A:Gene: GDB:TPS1
A:Cross-references: GDB:125890; OMTM:191080
A:Map position: 16pter-16qter

Db 131 ValAsnValSerSerHisValHisHisThrValThrLeuProProAlaSerGluThrPhePro 150
 OY CCGGGGATGGCGTGTGGGTCACCTGGCGGGGGGATGGGCAATGATGAGCCGCTCCCA 438
 OY ProGlyMetPProCysTyrValThrGlyTrrPglYAsPValAsPAsPAsPglUArgLeuPro 170
 OY 439 CCGCCATTTCCCTGAAAGCAGGTGAAGGTCCCAATATGAAACCAATTTGTTGACGCA 498
 Db 171 ProPrrPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190
 OY 499 AATATPCACCTTGGCGGCTACACGGGAGAGACAGCTCCGATTCGTCGACGACATGGCTG 558
 Db 191 LysTyrHisLeuGlyAlaTyrThrGlyAsPAsPValArgIleValArgAsPAsPmetLeu 210
 OY TGTGCGGGGAACCCCGGAGACTCATGACAGGGGCGATGTCGGGCGCCCTGGTGTGC 618
 Db 211 CysAlaGlyAsnThrArgArgAsPserCysGlnGlyAsPserGlyGlyProLeuValCys 230
 OY 619 AAGGTGAATGGCACCTGGCTGCAGCGGGCGTGTACAGCTGGGCGGAGGCTGTGCCAG 678
 Db 221 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyCysAlaGln 250
 OY 679 CCGAACCAGCGCTGGATGTACACCCCGTGTACCTACTACTGTTGGACTGGATCCACCATAT 738
 Db 251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAsPTrpIleHisHisTyr 270
 OY 739 GTCGCCAATAAAGCCG 753
 Db 271 ValProLysLysPro 275
 RESULT 3
 Cys583
 tryptase (EC 3.4.21.59) III precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Jun-2001
 C:Accession: G35863; A35863; A38893
 R:VanderSlige, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
 Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
 A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
 A:Reference number: A35863; MUID:90251647; PMID:2187193
 A:Accession: G35863
 A:Molecule type: mRNA
 A:Residues: 9-275 <VIAN>
 A:Accession: A35863
 A:Molecule type: DNA
 A:Residues: 1-9 <AA2>
 A:Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g3339977
 A:Note: The first nine residues of this sequence are inferred from genomic DNA of trypta
 R:VanderSlige, P.
 submitted to GenBank, April 1990
 A:Accession: A38893
 A:Molecule type: mRNA
 A:Residues: 9-131, 'K', 132-275 <VA3>
 A:Cross-references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID:g3339985
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine protease; zymogen
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-30/Domain: activation peptide #status predicted <ACT>
 F:31-275/Product: trypsin I #status predicted <MAT>
 F:31-267/Domain: trypsin homology <TRY>
 F:74,121,224/Active site: His, Asp, Ser #status predicted

Alignment Scores:
 Pred. No.: 1.09e-84 Length: 275
 Score: 1339.00 Matches: 240
 Percent Similarity: 97.96% Conservative: 0
 Best Local Similarity: 97.96% Mismatches: 5
 Query Match: 91.84% Indels: 0
 DB: Gaps: 0
 US-09-598-982-20 (1-771) x C35863 (1-275)

OY 19 ATGTCGGGGTCAAGAGGCCCCAGAGCAAGTGGCCCTGGACAGTGGCTGAGACTC 78
 Db 31 IleValGlyGlnGlnLalaPrrArgSerLysTrpProTrpGlnValSerLeuArgVal 50
 OY 79 CAGGCGCCATCTGGATGACCTTGTGGCGGGGCTCCATPCACCCGACCTGGCTGC 138
 Db 51 ArgAsPArgTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 70
 OY 139 ACCGCGCGGGCGTGGTGGAGCCGAGCTCAAGATCTGGCCCGCCCTGAGGGTGAAGT 198
 Db 71 ThrAlaAlaHisCysValGlyProAsPValLysAsPLeuAlaIleAlaArgValGlnLeu 90
 OY 199 CCGGAGCAGCACCTTACTTACCAGAGCACAGCTGCGCCGCGGACAGGATGCTGGTGC 258
 Db 91 ArgGlnGlnHisLeuTyrTyrGlnAsPValProValSerArgIleIleValHis 110
 OY 259 CCACAGTTCACACCCGCAAGATCGGAGCCGACATCGCCCTGTGAGACTGGAGAGCCG 318
 Db 111 ProGlnPheTyrThrAlaGlnIleGlyAlaAsPLeuIleLeuGlnIleuGlnIleuPro 130
 OY 319 GTGAAGTCTCCAGCCAGCTGCACACGGTACACCTGGCCCTGCTGAGACCTTCCG 378
 Db 131 ValAsnValSerSerHisValHisHisThrValThrLeuProProAlaSerGluThrPhePro 150
 OY 379 CCGGGGATGGCGTGTGGGTCACCTGGGCGGATGTGGCAATGATGAGCGCCCTCCCA 438
 Db 151 ProGlyMetPProCysTyrValThrGlyTrrPglYAsPValAsPAsPAsPglUArgLeuPro 170
 OY 439 CCGCCATTTCCCTGAAAGCAGGTGAAGGTCCCAATATGAAACCAATTTGTTGACGCA 498
 Db 171 ProPrrPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190
 OY 499 AATATPCACCTTGGCGGCTACACGGGAGAGACAGCTCCGATTCGTCGACGACATGGCTG 558
 Db 191 LysTyrHisLeuGlyAlaTyrThrGlyAsPAsPValArgIleValArgAsPAsPmetLeu 210
 OY 559 TGTGCGGGGAACCCCGGAGACTCATGACAGGGGCGATGTCGGGCGCCCTGGTGTGC 618
 Db 211 CysAlaGlyAsnThrArgArgAsPserCysGlnGlyAsPserGlyGlyProLeuValCys 230
 OY 619 AAGGTGAATGGCACCTGGCTGCAGCGGGCGTGTACAGCTGGGCGGAGGCTGTGCCAG 678
 Db 221 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyCysAlaGln 250
 OY 679 CCGAACCAGCGCTGGATGTACACCCCGTGTACCTACTACTGTTGGACTGGATCCACCATAT 738
 Db 251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAsPTrpIleHisHisTyr 270
 OY 739 GTCGCCAATAAAGCCG 753
 Db 271 ValProLysLysPro 275
 RESULT 4
 A45754
 tryptase (EC 3.4.21.59) alpha precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
 C:Accession: A45754; B37193
 R:Miller, J.S.; Westlin, E.H.; Schwartz, L.B.
 J. Clin. Invest. 84, 1188-1195, 1989
 A:Title: Cloning and characterization of complementary DNA for human tryptase.
 A:Reference number: A45754; MUID:90009311; PMID:2677049
 A:Accession: A45754
 A:Molecule type: mRNA
 A:Residues: 1-274 <MIT>
 A:Cross-references: GB:M30038
 R:Miller, J.S.; Moxley, G.; Schwartz, L.B.
 J. Clin. Invest. 86, 864-870, 1990
 A:Title: Cloning and characterization of a second complementary DNA for human tryptas
 A:Reference number: A37193; MUID:90369005; PMID:2203827
 A:Accession: B37193
 A:Molecule type: mRNA

A:Residues: 1-274 <MI2>
A:Cross-references: GB:M30038
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pro
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine protease; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-274/Product: trypsin I #status predicted <MAT>
F:74,120,223/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 2,34e-77 Length: 274
Score: 1232.50 Matches: 220
Percent Similarity: 92.65% Conserved: 7
Best Local Similarity: 89.80% Mismatches: 17
Query Match: 84.53% Indels: 1
Gaps: 1

US-09-598-982-20 (1-771) x A45754 (1-274)

Oy 19 ATCGTGGGGGTCAGAGAGCCCGCCAGGCAAGTGGCCCTGGAGGTGAGCCCTGAGATC 78
|||
Db 31 lIeValGIgYgInGluAlARoARgSerIySTRPrOTPrGInValSerLeuARgVal 50
Oy 79 CACGGCCCAATGACCTTCTGGGGGGGCGCCCTCATCCAGCCCGAGTGGGTG 138
|||
Db 51 ArgspARgIYTRrPMethIshPheCysGIdYgIserLeuIleHISPrGInlTRPValLeu 70
Oy 139 ACCGCCGGGGCGTGGGAGCAGCCGACGTCAGAGATCTGGCCCGCCCTGAGGTCAGACTG 198
|||
Db 71 ThrAlaAlaHIScYsLeuGIYrProARpYAlIlySAspLeuAlARHrLeuARgValAsn--- 89
Oy 199 CGGGAGCAGCACTACTACTACAGACGACGTCGTCGGGTCAGCAGGATGATGCTGAC 258
|||
Db 90 SerGIYThrHISLeuYrYrGIAspIdmLeuLeuProValSerARgIleMetValHIS 109
Oy 259 CCAGATTCATACACCGCCAGATGATGACGACATCCGCTGCTGGAGCTGGAGAGCCG 318
|||
Db 110 ProGInPrHeYrIleIleGInThrGIYAlaAspIleAlaLeuLeuGIuGIuPrO 129
Oy 319 GTGAGGTCTCCAGACGACGTCAGAGCTGACCGCTGGCCCTGCTGAGAGACTTCCCG 378
|||
Db 130 ValAsnIleSerARgValYAlHISrThrValMetLeuPrOProAlASerGIuThrPhePro 149
Oy 379 CCGGGGATGGCGTGGGTGACAGTGGGGGGCGATGTGACATGATGAGCGCTCCCA 438
|||
Db 150 ProGIYMePrOCySTRPValThrGIYTRPIdYAspValAspAsnAspGIuPrOleuPro 169
Oy 439 CCGCCATTTCCCTGAGAGCAGGTGAAGGTCCTCCATATGGAANAACATTTGTGACGCA 498
|||
Db 170 ProPrORPrOleuYgInValYValYValProIleMetGIuAsnHISleCysAspAla 189
Oy 499 AAARACACCTGGGGCTTACAGGGAGAGAGCAGCTCCGACATCTGTCGAGACATGCTG 558
|||
Db 190 LySTRYHISLeuGIYAlARyYrThrGIYAspAspYAlARgIleIleARgAspAspMetLeu 209
Oy 559 TGTGCGGGGAAACACCGGAGGACTGATGCCAGGGGACATCCCGGAGGGCCCTGGTGTGC 618
|||
Db 210 CysAlaGIYAsnSerGIuARgAspSerCysIySIdYAspSerGIYGIYProLeuValCys 229
Oy 619 AAGGTGATGACACCTGGCTGACAGCGGGCGTGGTCAAGTGGGGGAGAGGCTGTGCCAG 678
|||
Db 230 LySValAsnGIYThrTRPLeuGIuAlaGIYAlaYValSerTRPAspGIuGIYCyAlaGIu 249
Oy 679 CCACACCGGCTGGCAGTACACCCGCTGTCACCTGATGATGATGATGATGATGATGAT 738
|||
Db 250 ProAsnARgProGIYIleYrThrARgValYAlARyYrIleuAspTRPleHISrYr 269
Oy 739 GTCCCAAAAAAGCGG 753
|||
Db 270 ValProIySlySPro 274

RESULT 5
A38654
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
C:Accession: A38654; B38654; D35646; I59478
R:Reynolds, D.S.; Gunley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A:Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by
A:Reference number: A38654; MUID:91139682; PMID:1995658
A:Accession: A38654
A:Molecule type: DNA
A:Residues: 1-276 <REV>
A:Cross-references: GB:M57625; NID:q200506; PIDN:AAA39987.1; PID:q200507
A>Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 3
S GY, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 165 as Gly
A:Accession: B38654
A:Molecule type: mRNA
A:Residues: 1-276 <RE2>
A:Cross-references: GB:M57626; NID:q200508; PIDN:AAA39988.1; PID:q200509
R:Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A:Title: Different mouse mast cell populations express various combinations of at least
A:Reference number: A35646; MUID:90222202; PMID:2326280
A:Accession: D35646
A:Molecule type: protein
A:Residues: 32-54 <RE3>
R:Hung, R.; Adirlik, M.; Gohl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson
Scand. J. Immunol. 38, 359-367, 1993
A:Title: Expression of a mast cell typtase in the human monocytic cell lines U-937 a
A:Reference number: I59478; MUID:94023807; PMID:8210998
A:Accession: I59478
A:Status: preliminary; translated from GB/EMBL/DBD1
A:Molecule type: mRNA
A:Residues: 1-276 <RES>
A:Cross-references: GB:L31853; NID:q473480; PIDN:AAA39725.1; PID:q473481
C:Genetics:
A:Gene: M MCP-6
A:Introns: 24/1; 79/2; 168/1; 222/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine protease; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-31/Domain: activation peptide #status predicted <ACT>
F:32-276/Product: mast cell proteinase 6 #status experimental <MAT>
F:75,122,225/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 1.11e-67 Length: 276
Score: 1092.00 Matches: 192
Percent Similarity: 84.80% Conserved: 20
Best Local Similarity: 76.80% Mismatches: 36
Query Match: 74.90% Indels: 2
Gaps: 1

US-09-598-982-20 (1-771) x A38654 (1-276)

Oy 4 CCCCTCAGAAAADA-----ATCGTGGGGGTCAGAGAGCCCGCCAGGCAAGTGGCC 57
|||
Db 25 ProAlaAsnGInARgValGIYIleValGIYHISGIuAlaSerGIuSerIySTRPrO 44
Oy 58 TGGCAGGTGAGCCTGAGAGTCCACAGCGCCCATACTGATGATGATGATGATGATGATGAT 117
|||
Db 45 TrGIuValSerLeuARgPrHeIySLeuAsnTYrTRPleHISPhcYsGIYGIYSerLeu 64
Oy 118 ATCCACCCCGAGTGGGTGACCCCGCGGCGTGGTGGAGCCGACGTCAGAGATCTG 177
|||
Db 65 IleHISPrOGIuInTRPValLeuThrAlaAlaHIScYsValGIYPrOHISrIleYsSerPro 84
Oy 178 GCCGCCCTCAGGGTGCACACTGCGGGAGACAGCCTCTACTACAGACGACGCTGCTGCCG 237
|||
Db 85 GIuLeuPrHeARgValGIuLeuARgGIuGIuTYrLeuTYrGIYAspGIuLeuSer 104

OY	238	GTACAGAGATGATGTCGTCACCCAGCTTTACACC	GGCCAGATGCGAGCGGACATCCGC	297
DB	105	LeuAsnArg1IleValIleHisProHisTyrThrAlaIleGlyAlaIAspValAla	124	
OY	298	CTGCTGGAGCTGGAGAGCCGGTGAAGTTCACACC	AGCTTCACACGGTCAACCCTGCC	357
DB	125	LeuLeuGluLeuGluValProValAsnValSerThrHisIleHisProIleSerLeuPro	144	
OY	358	CTGCGCTAGAGACCTTCCCGCCGGGAGTATGCC	CTGGGTCACTGGCTGGGGGCGATGTG	417
DB	145	ProAlaSerGluThrPheProProGlyThrSerCysT	TrpValThrGlyTyrPheLysPheIle	164
OY	418	GACAATGATGAGCCGCCCTCCACCCGCAATTTCC	TCTGAACAGCAGGTGAAGTCCCAATATG	477
DB	165	AspAsnAspGluProLeuProProProProProP	roTyrProLeuLysGlnValLysValProIleVal	184
OY	478	GAAAACCAATTTGTGAGCGCAAAATACCACCTT	GGCGCTACAGCGGAGAGACAGCTCCGC	537
DB	185	GluAsnSerLeuCysAspArgTyrTyrHisThrG	lyLeuTyrThrGlyAspAspPhePro	204
OY	538	ATGTCGCTGACGACATGCTGTGTCCGGAGAAC	ACCCGGGAGGAGCTCATGGCCAGGGCGGC	597
DB	205	IleValHisAspGlyMetLeuCysAlaGlyAsn	ThrArgAlaArgAspSerCysGlnGlyAsp	224
OY	598	TCGGAGAGCCCTGTGCTGCAAGGTGAATGGC	ACCTGGCTGCACAGCGCGCGTGGTCAAC	657
DB	225	SerGlyGlyProLeuValCysLysValLysGly	ThrTyrPheGlnAlaGlyValValSer	244
OY	658	TGGGCGAGGCGGTGTGCCACAGCCGCTGGCAT	TACACCCGGTCAACCCGTCACTACAC	717
DB	245	TrrGlyGluGlyCysAlaGlnProAsnLysPro	GlyIleTyrThrArgValThrTyrTyr	264
OY	718	TTGACCTGATCCACCACTATGTCCCAAA	747	
DB	265	LeuAspTrpIleHisArgTyrValProGlu	274	
RESULT 6				
A32410				
C:Species:	Canis lupus familiaris (dog)			
C>Date:	12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999			
C:Accession:	A32410			
R:VanderSlite, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.				
Biochemistry	28, 4148-4155, 1989			
A:Title:	Molecular cloning of dog mast cell tryptase and a related protease: structural			
A:Reference number:	A32410; MUID:89352460; PMID:2504277			
A:Accession:	A32410			
A:Molecule type:	mRNA			
A:Residues:	1-275 <VAN>			
C:Superfamily:	trypsin; trypsin homology			
C:Keywords:	hydrolyase; serine protease; zymogen			
F:1-21/Domain:	signal sequence #status predicted <SIG>			
F:22-30/Domain:	activation peptide #status predicted <ACT>			
F:31-275/Product:	trypsin #status predicted <MAT>			
F:31-267/Domain:	trypsin homology <TRY>			
F:74,121,224/Active site:	His, Asp, Ser #status predicted			
Alignment Scores:				
Score:	1.2e-66	Length:	275	
Percent Similarity:	1077.00	Matches:	189	
Best Local Similarity:	85.71%	Conservative:	21	
Query Match:	77.14%	Mismatches:	35	
DB:	73.87%	Indels:	0	
Gaps:	2	Gaps:	0	
US-09-598-982-20 (1-771) x A32410 (1-275)				
OY	19	ATGCTGGGGGCTCAGGACCCCGAGAGAGTGCC	CGCTGGAGTGAAGCTTGAGAGTC	78
DB	31	IleValIleGlyArgAlaGlyAlaProGlySerLys	TrpProIleGlnValSerLeuArgLeu	50
OY	79	CACGGCCATACCTGGATCTTCGCGGGGCTCC	CTCCTATCCACCCCGAGTGGGTGCTG	138

DB	51	LysGlyIleTyrTrpArgHisIleCysGlySerLeu	IleHisProGlnThrPheValLeu	70
OY	139	ACCAGCCGGGGGCGCTGGTGGAGACCGGACG	TCGAAAGTCTGGCCCTAGGGTCAACTG	198
DB	71	ThrIleAlaHisCysValAlaGlyProAsnVal	ValCysProGluGluIleArgValGlnLeu	90
OY	199	GCGAGACACCTCTACTACCAGGACGACGCT	GCGCCGGTCAAGCAGGATCATGCTGGCAC	258
DB	91	ArgGluGlnHisLeuTyrTyrGlnAspHisLeu	LeuProValAsnArgIleValIleMetHis	110
OY	259	CCACAGTTCTACACCCCGCCAGATCGGAGCG	AGACATGGCCCTCTGGACCTGGAGGCGG	318
DB	111	ProAsnTyrTyrThrProGluAsnGlyAlaSpr	ileAlaLeuIleGluIleAsnPro	130
OY	319	GTAAGGTCTCCAGCCAGTCCACACCGTCA	CCCTGGCCCTCGCTCAGACACTTCCCC	378
DB	131	ValAsnValSerAlaHisValGlnProVal	ThrLeuProProAlaLeuGlnThrPhePro	150
OY	379	CCGGGATGCCGCTGGGTCTACTGGCTGGGG	CGATGTGGACATGATGAGCGCTCCCA	438
DB	151	ThrGlyThrProCysTrrValThrGlyTrrP	glyAspValHisSerGlyThrProLeuPro	170
OY	439	CCGCAATTTCTCTGAACAGGTGAAGTCC	CCCATATGAAACCACTTTGTGACGCA	498
DB	171	ProProPheProLeuLysGlnValLysVal	ProIleValGluAsnSerMetCysAspVal	190
OY	499	AAATACCACTTGGCGCTTACACGGGACAC	AGCACTGCCGATCGTGGACAGCACTGCTG	558
DB	191	GlnTyrHisIleGlyLeuSerThrGlyAsp	GlyValArgIleValAlaArgIleGluAspMetLeu	210
OY	559	TGTGCGGGAAACACCCCGAGGACTCATG	CCAGGGCGACTCCGAGGGCCCTGGTGTGC	618
DB	211	CysAlaGlyAsnSerLysSerAspSerCysGln	LysAspSerGlyGlyProLeuValCys	230
OY	619	AAGGTGAATGGCACCCTGCAGCGGGCG	GTGTCAGCTGGGGGAGGGCTGTGCCCG	678
DB	231	ArgValArgGlyValTrrPheGlnAlaGly	ValIleSerTrrPglyGluCysAlaGln	250
OY	679	CCCAACCGCCCTGGGATGTACACCCGCT	GTCCACTACTTGGACTGGATGCCACACAT	738
DB	251	ProAsnArgProGlyIleTyrThrArgVal	AlaTyrTyrLeuAspTrrIleHisGlnTyr	270
OY	739	GTCGCCAAAAAGCCG	753	
DB	271	ValProLysGluPro	275	
RESULT 7				
S56160				
C:Species:	Meriones unguiculatus (Mongolian jird)			
C>Date:	27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000			
C:Accession:	S56160			
R:Murakumo, Y.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.				
Biochem J	309, 921-926, 1995			
A:Title:	Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Merione			
A:Reference number:	S56160; MUID:95366971; PMID:7639711			
A:Accession:	S56160			
A:Status:	Preliminary			
A:Molecule type:	mRNA			
A:Residues:	1-270 <MUR>			
C:Superfamily:	KMBL:D31789; NID:9517122; PIDN:BAA06598.1; PID:9517123			
F:26-262/Domain:	trypsin homology <TRY>			
Alignment Scores:				
Score:	1.64e-66	Length:	270	
Percent Similarity:	1075.00	Matches:	188	
Best Local Similarity:	84.77%	Conservative:	18	
Query Match:	77.37%	Mismatches:	37	
DB:	73.73%	Indels:	0	
Gaps:	2	Gaps:	0	

US-09-598-982-20 (1-771) x S56160 (1-270)

19 ATGTCGGGGGGTCAAGAGCCCGCCAGAGCAAGTGGCCCTGGAGTGGAGTGC 78
26 IValaIGlyGInGInGInaLarProGlyAsnLysTrpProTrpGInValaSerLeuYrGala 45
79 CAGCGCCCAATCACTGGATCTGGCGGGGGCTCCCTATGCCAAGCCAGTGGGTCTG 138
46 AsnGIuPrlrYrTrpArGInHisPheCysGlyGlySerLeuIleHisProCInDrPrValLeu 65
139 ACCGGCCGGCGGTGGCTGGAGCCGGAGCTCAAGATCTGGCCCGCCCTGAGGCTGACTG 198
66 ThrIlaaLanHisCysValaGlyProThrIleAlaAsnProAsnLysValaArgValaGInLeu 85
199 CGGAGGAGCAAGCTACTATACAGAGCCAGAGCTGGCGGGCGGAGGAGGATGATGGTGCAC 258
86 ArgLysGInLysLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 105
259 CCACAGTCTCTACACCCCGCCAGATCGAGAGCCAGATCGCCCTGGCTGGAGCTGGAGCCG 318
106 ProTrpIrrheYrAlaTrpGInaAsnGlyAlaAsnIleAlaLeuLeuGInLeuLysAsnPro 125
319 GTGAAGTCTCCAGCCAGCTCCACAGGCTCAACCCCTGGCTCAAGAGCTGGTCCC 378
126 ValAsnIleSerSerHisValHisIleProValSerLeuProProAlaSerGlyUtrPhePro 145
379 CCGGGGATCCCGTGGTGGTACATGGCTGGGGCGATGGTGGAGCAATGATGAGGCCCTGCCA 438
146 SerGlyUtrLeuCysTrpValTrpGlyTrpGlyAsnIleAsnAsnAsnValSerLeuPro 165
439 CCGCATTTCTCTATACACAGGAGTGAAGTCCCGCCATGAATGGAAGGATTTGTGGAGCA 498
166 PropProIrrheProLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys 185
499 AAATTCACACCTGGGGCCCTACACGGGAGACAGACCTCCGATCGTCCGTPAGACACTGG 558
186 LysTrpYrHisLysGlyValLysTrpGlyAsnAsnIleHisIleValaIArgAsnAsnMetLeu 205
559 TGTGGCGGGAACACCCCGGAGGACTCATGCCAGCGGAGCTCCGAGGGCCCTGGTGTGC 618
206 CysAlaIArgLysAsnGlyLysAsnSerCysGlnGlyAsnSerGlyGlyProLeuValCys 225
619 AAGTGAATGGCAGCCCTGGCTGCAGCGGGCGGTGTCACTGGGGCGAGGGCTGTGCCAG 678
226 LysValaAsnGlyTrpTrpLeuGlnAlaGlyValaIleValaIleSerTrpGlyUclYcysAlaLeu 245
679 CCGAAGCCGGCTGGAGTGTACACCCGCTGACCTACTGACTGGATGGATGCCACCACTAT 738
246 ProAsnArgProGlyLysLeuTrpIrrheValTrpYrLysLeuAsnPrpIleHisArgYr 265
739 GTCGCCAAA 747
266 ValProLys 268

RESULT 8
A47246
tryptase (EC 3.4.21.59) 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A47246
R:McNeill, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurtley, D.S.; Austen, K.F.;
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A:Title: Isolation, characterization, and transcription of the gene encoding mouse mast
A:Reference number: A47246; MUID:93087489; PMID:1454796
A:Accession: A47246
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-273 <MNC>
A:Cross-references: GB:I00653; NID:9200518; PIDN:AAA39992.1; PID:9200519
C:Superfamily: tryptsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:29-265/Domain: trypsin homology <NRY>

Alignment Scores:
Pred. No.: 2,85e-65 Length: 273
Score: 1057.00 Matches: 189
Percent Similarity: 82.07% Conserved: 17
Best Local Similarity: 75.30% Mismatches: 43
Query Match: 72.50% Gaps: 2
DB: 1

US-09-598-982-20 (1-771) x A47246 (1-273)
QY 1 GGGCCCTCGAAGAAAGA-----ATGTCGGGGGGTCAAGAGCCCGCCAGAGCAAGTGG 54
DB 21 GLYProAlaMetThrArgGlnGlyIleValaGlyGlnGlnaLanHisGlyAsnLysTrp 40
QY 55 CCGTGGGAGGAGCTGGAGCTGGAGCCCGCCATAGCGATGGATGGCACTGGCGGGGGCTCC 114
DB 41 ProTrpGInValaSerLeuArgAlaAsnAsnPrpTrpYrTrpPheIleHisPheCysGlySer 60
QY 115 STCAITCCACCCCGAGTGGCTGGAGCCCGCCGGCTGGCTGGAGCCCGCCAGAT 174
DB 61 LeuIleHisProGlnIrrPrValLeuTrpAlaHisCysValaGlyProAsnValaIlaAsp 80
QY 175 CTGGCCCGCTCAAGGGCTCAAGCTGGAGGAGGAGCAGCCTACTACTCAAGAGCAAGCTGG 234
DB 81 ProAsnLysValaArgValaGlnLeuAlaArgLysGlnTrpYrLysLysAsnIleMet 100
QY 235 CCGGTCACAGGATCATCTGGCTGGAGCCCGCCAGTTCACACCCCGCCAGTCCGGAGCAGATC 294
DB 101 ThrValSerGlnIleIleTrpHisProAsnPrpHeYrIleValaGlnAspGlyAlaAspIle 120
QY 295 GCGCTGTGGAGCTGGAGGAGCCCGGTGAAGTCTCCAGCCAGTCCACAGCCGTCAGCCCTG 354
DB 121 AlaLeuLeuLysLeuTrpAsnProValaAsnIleSerIleAsnArgYrValaIrrheProLeu 140
QY 335 CCGCCCTGGCTCAAGAGCTGGAGCCCGGGGAGTCCGCTGGTGGTGGTGGCTGGGGGGAT 414
DB 141 PropProAlaSerGlnTrpPheProSerGlyTrpLeuCysTrpValTrpGlyTrpGlyAsn 160
QY 415 GTGGACAAATGATGAGCCCTGGCTCCAGCCCGCCATTTCTTGAAGCAGAGTCAAGCTCCCA 474
DB 161 IleAsnAsnGlyValaAsnLeuProProIrrheProLeuLysGlnValaGlnValaProIle 180
QY 475 ATGGAAGAACCAACATTTGTAGCAGCAAAATATACACCTGGCGCCCTACAGCGGAGCAGC 534
DB 181 IleGluAsnHisLeuCysAspIrrheLysTrpYrHisLysGlyLeuIleTrpGlyAspAsnVal 200
QY 535 CGCATCTGCTGGAGCAGATGCTGTGTGGCGGGAACACCCGGAGGAGTCACTATGCCAGGGC 594
DB 201 HisIleValaIArgAsnAspMetLeuCysAlaGlnLysAsnGlnGlyLysAsnSerCysGlnGly 220
QY 595 GACTCCGGAGGGCCCTGGCTGGCAAGGTGAATGAGCAGCAGCTGGCTGCAGAGCGGGCTGG 654
DB 221 AspSerGlyGlyProLeuValCysLysValaGlnAsnPrpTrpLeuGlnAlaGlyValaVal 240
QY 655 AGCTGGGGGAGGGCTGTGCCAGCCCAAGCCCGCTGGAGTCTACAGCCCGTGTCACTAG 714
DB 241 SerTrpGlnGlyGlnGlyCysAlaIleInProAsnArgProGlyIleYrTrpArgValTrpYr 260
QY 715 TACTTGGAGCTGGATCCAGCACTATGTCGCCAAA 747
DB 261 TyrLeuAsnPrpIleHisIleHisIleValaProLys 271

RESULT 9
JC4171
tryptase (EC 3.4.21.59) precursor - rat
N:Alternate names: mast cell tryptase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C:Accession: JC4171
R:Idé, H.; Itoh, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.; Osada, Y.
J. Biochem. 118, 210-215, 1995
A:Title: cDNA sequencing and expression of rat mast cell tryptase.

A:Reference number: J04171; MUID:96015171; PMID:8657314
 A:Accession: J04171
 A:Molecule type: mRNA
 A:Residues: 1-274 <IDE>
 A:Cross-references: DDBJ:D38455; NID:9556555; PTDN:BA07486.1; PID:9556555
 C:Comment: This enzyme is basically specific for a connective tissue mast cell, it is up
 enase inhibitors.
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-29/Domain: activation peptide #status predicted <ACT>
 F:30-274/Product: mast cell trypsin #status predicted <MTR>
 F:30-286/Domain: trypsin homology <TRY>
 F:73,120,223/Active site: His, Asp, Ser #status predicted
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 3,92e-65 Length: 274
 Score: 1055.00 Matches: 187
 Percent Similarity: 84.06% Conservative: 24
 Best Local Similarity: 74.50% Mismatches: 38
 Query Match: 72.36% Indels: 2
 Gaps: 1
 US-09-598-982-20 (1-771) x J04171 (1-274)

```

  QY  4  CCCCTCGAAGAAAGA-----ATCGTCGGGGTCAGAGAGGCCCCGAGGAGCAGATGGGCC 57
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  23  PrvAlaValSglnAlaValGlyYlLeValGlyValArgGlnAlaSerGlnSerLysLysTrpPro 42
  QY  58  TGGCAGGTGAGCCTCAGAGCCAGCCAGCAGGAGGAGGAGTGTGATGCACTTTCTGGGGCCCTCC 117
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  43  TrpIlnValSerLeuAlaArgPheLysPheSerPheThrPheMetHisPheCysGlyValSerLeu 62
  QY  118  ATCCAGCCGCGTGGGGTCAGAGCCGGCGGGGGCGGGCGGGAGGCGAGCCGTCAGAGATCTG 177
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  63  IlnHisProGlnTrpAlaLeuThrAlaLlnHisCysValGlyLlnHisLysLysSerPro 82
  QY  178  GCCCCCTCAGAGGTGAGCAGCTCAGGAGAGCAGCCTACTACTCAGGAGCCAGCAGCAGCTGTGCGG 237
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  83  GluLeuPheArgValGlnLeuArgGlnGlnIlnPheLysLysLysLysLysLysLysLysLysLys 102
  QY  238  GTCAAGCAGATCATGTGTCCACCCAGCTATCACAGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 297
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  103  ValAsnAlaTrpIlnValValAlnHisProHlsTrpLysTrpValGlnLysAspIlnLala 122
  QY  298  CTGCTGAGAGGTGGAGAGCCGGGTAAAGTCTCCACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 357
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  123  LeuLeuGlnLeuGlnLlnPheProValAlnSerTrpHisLlnHisProLlnSerLeuPro 142
  QY  358  CCTGCCCTCAGAGCCTTCCCTCCCGGGAGTGGCTGGGTGACCTGAGTGGGTGGGAGGAGTGTG 417
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  143  ProLlnSerGlnTrpIlnPheProSerGlyThrSerGlyTrpValIlnThrGlyTrpGlyLysAsp 162
  QY  418  GACAAATGATGAGCGCTCCGAGCCAGTTCCTGTCAAGCCAGTGAAGAGCCAGTGAAGTCCCATTAATG 477
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  163  AspSerAspGlnProLeuProLlnPheProLysLysLysLysLysLysLysLysLysLysLysLys 182
  QY  478  GAAAAACAATTTGTGAGCGCAAAATACCACCTGGCGGCTACAGCGGAGAGACAGAGCTCCGGC 537
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  183  GluLlnSerLeuCysAspArgLysTrpHisLlnPheLysLysLysLysLysLysLysLysLysLys 202
  QY  538  ATCTCCGTGAGCAGATGCTGTGTCCGGGAGAACCCGGGAGCAGCTATGGCAGAGGCGAGC 597
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  203  IlnValGlnAspGlyMetLeuCysAlnGlyAlnHisTrpHisSerAspSerCysGlnGlyAsp 222
  QY  598  TCCGAGGCGCCCTGTGTGTGCAAGTGAATGCACTCTGGCTGCAGAGCCGGCGGCTGGTCAAGC 657
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  223  SerGlyLysProLeuValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 242
  QY  658  TGGGCGAGGGCTGTGCCAGCCCAAGCCCAAGCCGCTGGCATACAGCCGCTGTGTACTACTAC 717
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  243  TrpGlyGlnGlyCysAlnGlnAlaAsnArgProGlyLlnPheValArgValLlnThrLysLys 262
  
```

OY 718 TTGGACTGATCCACACCTATGTCCCAAAAAG 750
 |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
 Db 263 LeuAspTrpIlnHisAspGlyValProGlnArg 273

RESULT 10
 568702
 trypsin (BC 3.4.21.59) - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
 C:Accession: S68702; S68676
 R:Palloero, M.; Gambacurta, A.; Fiorucci, L.; Mignogna, G.; Barra, D.; Ascoli, F.;
 Eur. J. Biochem. 237, 100-105, 1996
 A:Title: cDNA cloning and primary structure of trypsin from bovine mast cells, and e
 A:Reference number: S68676; MUID:96203914; PMID:8650861
 A:Accession: S68702
 A:Molecule type: mRNA
 A:Residues: 1-237 <PAL>
 A:Cross-references: EMBL:X94982; NID:91332446; PTDN:CAA64438.1; PID:91332447
 A:Accession: S68676
 A:Molecule type: protein
 A:Residues: TVGGQEAR, 1-8; 61-74; 90-97; 126-148; 162-190; 208-222; 227-235 <PAW>
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
 F:1-229/Domain: trypsin homology (fragment) <TRY>
 F:36,83,177/Active site: His, Asp, Ser #status predicted
 F:94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 1,09e-61 Length: 237
 Score: 1005.00 Matches: 178
 Percent Similarity: 84.32% Conservative: 21
 Best Local Similarity: 75.42% Mismatches: 37
 Query Match: 68.93% Indels: 0
 Gaps: 0
 US-09-598-982-20 (1-771) x S68702 (1-237)

```

  QY  46  AGCAAGTGGCCCTGAGAGGTGAGCCGTCAGAGCAGCCAGCAGCTGATGTCAGTCTGTC 105
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  2  SerIlnTrpProTrpGlnValSerLeuArgValSerArgArgLysTrpArgLysHisCys 21
  QY  106  GGGGGTCCCTCATCCACCCAGCCAGTGGGTGTCAGCCGGCGGCGGGCGGGAGCCAGC 165
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  22  GlyGlySerLeuLlnHisProGlnTrpValLlnPheAlaAlnHisCysValGlyProGln 41
  QY  166  GTCAAGATCTGCCCGCCCTCAGAGCAGTGGTGGAGCAGCAGCAGCTACTACAGAGAC 225
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  42  ValHisGlyProSerLysPheArgValGlnLeuArgGlnLlnHisLysLysLysLysLysLysLys 61
  QY  226  CAGTGTGCGCGGTGAGAGATATGTCAGCCACAGTTCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 285
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  62  GlnLeuLeuProLlnSerArgLlnPheProHisProAsnCysLysValLysAsnGly 81
  QY  286  GCGGACATCCGCTGTGGAGGTGGAGAGCCGGTGAAGTCTCAGCCAGCCAGCCAGCCAGCCAGCCAG 345
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  82  AlaAspIlnAlaLeuLeuGlnLeuAspArgLysLysLeuValAlnLlnSerTrpHisValGlnPro 101
  QY  346  GTCAAGCAGTCCCGCCTCAGAGACCTTCCCGCGGGAGATGCCGTGTGGTGTGACTGGC 405
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  102  ValThrLeuProProGlnSerGlnTrpPheProProGlyThrGlnCysTrpValLlnThrGly 121
  QY  406  TGGGGAGATGGAGCAATGATGAGCCGCTCCAGCCAGTTCCTGTGAAGCAGAGTGAAG 465
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  122  TrpIlnAsnValAspAsnGlyArgArgLysLeuProProPheProLysLysLysLysLysLysLys 141
  QY  466  GTCCCAAATATGAAAACACATTTGTGACCGCAAAATACCACCTGGCGGCTACAGCCAGC 525
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  142  ValProValValGlnAsnSerValCysAspArgLysTrpHisSerGlyLysSerThrGly 161
  QY  526  GAGCAGCTCCGATGTCTCCAGCAGATGCTGTGTCCGGGAGAACCCGGGAGGACTCA 585
     |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||  |||:|||||:|||||
  Db  162  AspAsnValProLlnValArgGlnAspMetLeuCysAlnGlyAspSerGlyArgAsnPhe 181
  
```


QY 481 AACCAATTTGTGACGAAATAATACCCCTTGGCCCTACACGGGAGACGACGCTCCGAC 540
 DB 180 AsnAaGgIuCySAsnCySHisTyrIln-----PhrIleuGluGlnAspAspIuVal 197
 QY 541 GTCGTCGACGACATGCTGTGTGGCCGGAAACACCCGGAGGACTATGCCAGGGCCACTCC 600
 DB 198 ILeYsGlnAspMethLeuCySAlaGlySerGluGlnHisAspSerCySglnMetAspSer 217
 QY 601 GGAGGGCCCTGTGTGTGGAAGGTGAATGGCAACCTGGCTGACGGGGGGGTGGTCAAGCTGG 660
 DB 218 GILgYrPrOleuValCyAaGlyTrpIlyScYshTrpIleGlnValGILyAlValSerTrp 237
 QY 661 GCGAGGGCTGTGTGCCCCAACCCGCGCTGGCATCTACCCCTGTGACTACTGCTGTG 720
 DB 238 GILyTrpIlyCySgILyTr-----AsnleuProGlyValIlyTrAlaArgValThrSerTrpVal 256
 QY 721 GACTGGATGCCACATATGATGTCGCCCAAAAAGCGG 753
 DB 257 serTrpIleHisGlnHisIleProleuSerPro 267

RESULT 13

A57014
 prostaasin (EC 3.4.21.-) precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 18-Jun-1999
 C:Accession: A57014; A54866
 R:Yu, J.X.; Chao, L.; Chao, J.
 J. Biol. Chem. 270, 13483-13489, 1995
 A:Title: Molecular cloning, tissue-specific expression, and cellular localization of hum
 A:Reference number: A57014; MUID:95286644; PMID:7768952
 A:Accession: A57014
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-343 <RES>
 A:Cross-references: GB:L1351; NID:9862304; PIDN:AAC41759.1; PID:9862305
 A:Experimental source: prostate
 A:Note: parts of this sequence were determined by protein sequencing
 R:Yu, J.X.; Chao, L.; Chao, J.
 J. Biol. Chem. 269, 18843-18848, 1994
 A:Title: Prostaasin is a novel human serine protease from seminal fluid. Purification,
 A:Reference number: A54866; MUID:94308140; PMID:8034638
 A:Accession: A54866
 A:Molecule type: protein
 A:Residues: 45-64 <YDA>
 C:Genetics:
 A:Gene: GDB:PRSS8
 A:Cross-references: GDB:676446; OMTM:600823
 A:Map position: 16p11.2-16p11.2
 C:Superfamily: prostaasin; trypsin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-44,45-343/Product: prostaasin #status predicted <MNT>
 F:33-44/Domain: prostaasin light chain #status predicted <CHL>
 F:45-343/Domain: prostaasin heavy chain #status predicted <CHH>
 F:45-281/Domain: trypsin homology <TRY>
 F:323-341/Domain: transmembrane #status predicted <TM1>
 F:37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
 F:85,134,238/Active site: His, Asp, Ser #status predicted
 F:159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:

Pred. No.: 9.61e-28 Length: 343
 Score: 512.00 Matches: 103
 Percent Similarity: 57.03% Conservative: 39
 Best Local Similarity: 41.37% Mismatches: 97
 Query Match: 35.12% Indels: 10
 DB: 1 Gaps: 6

US-09-598-982-20 (1-771) x A57014 (1-343)
 QY 10 GAGAAAGAAATGCTGGGGGTCAGAGGCGCCAGGACAGTGGCCCTGGCAGGTGAGC 69
 DB 42 GlnAlaArgIleThrGlyGlySerSerAlaValAlaGlyGlnTrpProTrpIlnValSer 61

QY 70 CTGAGAGTCSAAGCCSCAATCTGATGGACTTGTGGGGGGCTCCCTGATCCAGCCCGAC 129
 DB 62 ILeHrTrpGluGly-----ValHisValCySgILyGlySerLeuValSerIuGln 78
 QY 130 TGGGTCTGACCCCGCCGGCTGTGCTGGGAGCCGACGTCMAAGATCTGCCGCCCTCAGG 189
 DB 79 TrpValLeuSerAlaIlnHisCySphe---ProserGlnHisIlnIlyGluValLeTrpIu 97
 QY 190 CTGCAACTGGCCGGAGACACACACTC-----TACTCCAGAC--CACTGCTGCCGGT 240
 DB 98 ValIlySerGlyAlaIlnGlnIleuAspSerTrpSerGlyAspAlaIlyValSerThrIleu 117
 QY 241 AGCAGATCATGTGCTGACCCCAAGTCTTACACCCCGCCAGATCCGGAGACATCCCGCTG 300
 DB 118 LysAspIleIleProHisProSerTrpIleuGlnIlySerGlnIlyAspIleAlaIle 137
 QY 301 CTGAGACTGAGACGACCCCGGTGMAAGTCTCCAGCCACTCCACACGCTCACCCTGCCCT 360
 DB 138 LeuGlnLeuSerArgProIleThrPheSerArgTrpIleValGlyProIleCysIleuProAla 157
 QY 361 GCCTGAGACACTTGTCCCGGGGATGCCGCTGTGCTGCTGCTGGTGGGGGAGTGTGAC 420
 DB 158 AlaAsnAlaSerPheProAsnIlyLeuHisCysThrValIlnGlyTrpGlyHisValAla 177
 QY 421 AATGATGAGCCGCTCCCAACCCGATTCCTCTGGAAGGACGATCCCAATATGGA 480
 DB 178 ProSerValSerLeuThrProIlyProIlySerGlnIlnGlnIlnValProIleuIleSer 197
 QY 481 AACCAATTTGTGACGAAATAATACCCCTTGGCCCTACACGGGAGACGACGCTCCGACATC 540
 DB 198 ArgIuTrpIlyCySAsnCySLeuTrpIlyAsnIlnLeuAspAla---LysProGlnIlnProHisPhe 216
 QY 541 GTCGTCGACGACATGCTGTGTGGCCGGAAACACCCGG-----AGGCACTCATGCCAGGC 594
 DB 217 ValGlnGlnAspMetValCySAlaGlyTrpValGlnGlyGlyLysAspAlaCysGlnIly 236
 QY 595 GACTCCGGAGGGCCCTGTGTGGAAGGTAATGGCACTGCTGCTGACAGCCGGCGTGGTTC 654
 DB 237 AspSerGlyGlyProleuSerCysProValGlnGlyLeuTrpTrpIlyLeuIlnIlyVal 256
 QY 655 AGCTGGGGCGAGGCTGTGCCCAAGCCCAACCCGCTGCATCTACACCCGCTGCTCAGTAC 714
 DB 257 serTrpGlyAspAlaCysGlyAlaArgAsnArgProGlyValIlyTrpIleuAlaSerSer 276
 QY 715 TACTTGGACTGGATGCCACCACTATGTC 741
 DB 277 TyrAlaSerTrpIleGlnSerIlyVal 285

RESULT 14

KRHU1
 coagulation factor Xta (EC 3.4.21.27) precursor [validated] - human
 N:Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
 C:Species: Homo sapiens (man)
 C:Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-Dec-2000
 C:Accession: A27431; A00920; A37940
 R:Asakai, R.; Davie, E.W.; Chung, D.W.
 Biochemistry 26, 7221-7228, 1987
 A:Title: Organization of the gene for human factor XI.
 A:Reference number: A27431; MUID:88107663; PMID:2827746
 A:Accession: A27431
 A:Molecule type: DNA
 A:Residues: 1-625 <ASA>
 A:Cross-references: GB:M18295
 A:Note: the sequence shown follows the authors' translation
 R:Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
 Biochemistry 25, 2417-2424, 1986
 A:Title: Amino acid sequence of human factor XI, a blood coagulation factor with four
 A:Reference number: A00920; MUID:86243360; PMID:3636155
 A:Accession: A00920
 A:Molecule type: mRNA
 A:Residues: 1-625 <FDU>
 A:Cross-references: GB:M13142; NID:9182832; PIDN:AAA52487.1; PID:9182833

R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
 A:Title: Location of the disulfide bonds in human coagulation factor XI: the presence of
 Biochemistry 30, 2056-2060, 1991
 A:Reference number: A37940; MUID:91152017; PMID:1998667
 A:Accession: A37940

A:Molecule type: protein
 A:Residues: 28-33;35-46, 'X', 51-55, 'X', 57-63;70-75, 'X', 77-79;107-109, 'X', 111-112;132-139,
 ;280-282, 'X', 284;285-297;313-316, 'X', 318-319;320-326; 'X', 328-330; 'X', 347-349;373, 'X', 375
 C:Comment: The proenzyme consists of two identical chains linked by one or more disulfide
 he active site, and a heavy chain, which associates with high molecular weight (HMW) kit
 C:Genetics:
 A:Gene: GDB:F11
 A:Cross-references: GDB:119891; OMTM:264900
 A:Map position: 4q35-4q35
 A:Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor IX
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor XI; trypsin homology
 C:Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydr
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-387/Product: coagulation factor Xia heavy chain #status experimental <HCH>
 F:19-108/Domain: apple repeat <AP1>
 F:109-198/Domain: apple repeat <AP2>
 F:199-288/Domain: apple repeat <AP3>
 F:290-379/Domain: apple repeat <AP4>
 F:388-625/Product: coagulation factor XIA light chain #status experimental <LCH>
 F:388-618/Domain: trypsin homology <TRY>
 F:20-103,514-561,571-599/disulfide bonds: #status predicted
 F:29/Disulfide bonds: Interchain #status experimental
 F:46-76,50-56,110-193,136-156,140-146,200-283,226-295,230-236,291-374,317-346,321-327,38
 F:90,125,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:339/Disulfide bonds: Interchain #status predicted
 F:387-388/Cleavage site: Arg-Ile (coagulation factor XIra) #status experimental
 F:431,480,575/Active site: His, Asp, Ser #status predicted
 F:491/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment scores:
 Pred. No.: 1,18e-24 Length: 625
 Score: 467.00 Matches: 99
 Percent Similarity: 51.59% Conservative: 31
 Best Local Similarity: 39.29% Mismatches: 94
 Query Match: 32.03% Indels: 28
 Gaps: 6

US-09-598-982-20 (1-771) x KFHU (1-625)

Db 503 SerIysGlyAspArgAsnValIleTyrThrAspCysTrpValIThrGlyTrpGlyTyrArg 522
 Qy 412 -----GATGNGACCAAMGATGAGCGCTCCACCGCCATTTCTGTGAACAGC 459
 Db 523 LysLeuArgAspIysIleGlnAsn-----ThrLeuGlnIlys 534
 Qy 460 GTGAAGGTCCCCCAAMAGAAACACACATTTGTGACGCCAAMATACCACTTGGCGCCATC 519
 Db 535 AlAlYsIleProLeuValIThrAsnGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnu 554
 Qy 520 ACGGAGACAGACAGTCCCGATGCTCCCGTCCGACAGCATGCTGTCGGGGAGAACCCCGG--- 576
 Db 555 Thr-----HisLysMetIleCysAlaGlyTyrArgGlnuGly 566
 Qy 577 ---AAGCATATGATGACAGCGGACATCCGAGGCGCCCTGTGTGCAAGGTGAAGACAC 633
 Db 567 GlyLysAspAlaCysGlyGlyIAspSerGlyGlyProLeuSerCysLysHisAsnGluVal 586
 Qy 634 TGGCTGACGGCGGCGGTGTCAGCTGGGCGAGGGCTGTGCCCAACCGCGCCGTGGC 693
 Db 587 TrpHisLeuValGlyIleThrSerTrpGlyGlnuGlyCysAlaGlnuArgGluArgProGly 606
 Qy 694 ATCTAACCCCTGATCCACTACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 729
 Db 607 ValIlyTrpHisAsnValValGluTrpValAspTrpIle 618

RESULT 15
 KOHP
 plasma kallikrein (EC 3.4.21.34) precursor - human
 N:Alternate names: Kallinogenin; plasma prekallikrein
 C:Species: Homo sapiens (man)
 C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
 C:Accession: A00921; A37939
 R:Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
 Biochemistry 25, 2410-2417, 1986
 A:Title: Human plasma prekallikrein, a zymogen to a serine protease that contains fou
 A:Reference number: A00921; MUID:86243559; PMID:3521732
 A:Accession: A00921
 A:Molecule type: mRNA
 A:Residues: 1-638 <CHU>
 A:Cross-references: GB:M13143; NID:q190262; PIDN:AAA60153.1; PID:q190263
 R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
 Biochemistry 30, 2050-2056, 1991
 A:Title: Location of the disulfide bonds in human plasma prekallikrein: the presence
 A:Reference number: A37939; MUID:91152016; PMID:1998666
 A:Accession: A37939

A:Molecule type: protein
 A:Residues: 20-27;40-46, 'X', 48, 'H', 50, 'X', 52-70, 'H', 75-76, 'X', 78-80;103-113;131-140;1
 ;260-283, 'X', 285;287-291, 'X', 293-295;314-317, 'X', 319-320;321-324, 'X', 329-333;334-339,
 525;538-551;562, 'X', 564-567;573, 'X', 575-576;578-583, 'X', 585;592-604 <MCM>
 C:Comment: This protein, synthesized in the liver, circulates as a noncovalent comple
 C:Comment: The zymogen is activated by factor XIra, which cleaves the molecule into a
 are linked by one or more disulfide bonds.
 C:Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciproc
 Inogen and may also play a role in the renin-angiotensin system by converting proreni
 C:Genetics:
 A:Gene: GDB:K1K3
 A:Cross-references: GDB:127575; OMTM:229000
 A:Map position: 4q35-4q35
 C:Superfamily: coagulation factor XI; trypsin homology
 C:Keywords: blood coagulation; duplication; fibrinolytic; glycoprotein; hydrolase; in
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-638/Product: plasma kallikrein #status predicted <MAT>
 F:20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
 F:20-109/Domain: apple repeat <AP1>
 F:110-199/Domain: apple repeat <AP2>
 F:200-289/Domain: apple repeat <AP3>
 F:291-380/Domain: apple repeat <AP4>
 F:391-621/Domain: plasma kallikrein light chain #status predicted <LCH>
 F:391-621/Domain: trypsin homology <TRY>
 F:21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,
 F:121,308,396,453,494/Binding site: carbohydrate (asn) (covalent) #status experimen
 F:318-347,340-345/disulfide bonds: #status predicted

F:390-391/Clavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F:434,483,578/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 1.49e-23 Length: 638
Score: 451.00 Matches: 96
Percent Similarity: 54.40% Conservative: 40
Best Local Similarity: 38.40% Mismatched: 84
Query Match: 30.93% Indels: 30
DB: 1 Gaps: 8

US-09-598-982-20 (1-771) x K0HUP (1-638)

```
QY 16 AGAATCTGGGGGCTCAGAGGCCCCAGAGCAAGTGGCCCTGGCAGAGTGGAGTGA 75
   |||||
Db 390 ArgIleValGIgLYLThAsnSerTrrpLgLIuTrrPrroTrrpGIValSerLeuGI 409
QY 76 GTCCAGGCCCCATACSTGGATGCACTTGTGGGGGCTCCSTCATCCACCAGTGGG 135
   |||
Db 410 ValLysLeuThraLagLInArgHisLeuCySGIYSerLeuIleGIYHisGIInTrrpVal 429
QY 136 CTGACCCGGGGGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 192
   |||||
Db 430 LeuThraLalaLInLscYsrPheAspGIYLeuProLeuGIInAspVal-----TrrpArgIle 447
QY 193 CAA-----CTGCGGAGACAGCCTTACCTACAGAGCAGCAGCAGCAGCAGCAGC 243
   |||
Db 448 TyrSerGIYIleLeuAsnLeuSerAspIleThrLYLAspTrpIrrPheSerGIInIleLys 467
QY 244 AGGATCATGCTGACCCACAGTGTACACCCGACAGTGGAGTGGAGTGGAGTGGAGTGG 303
   |||||
Db 468 GluIleIleIleHisGIInAspTrpLYLValSerGIInLysValAsnHisAspIleLalaLeuIle 487
QY 304 GAGCTGGAGAGCCGGTGAAGGCTTCCAGCCAGCAGTCCAGCAGCAGCAGCAGCAGC 363
   ::|||
Db 488 LysLeuGIInAlaProLeuAsnTrpTrpIurPheGIInLysProIleCySLeuProSerLys 507
QY 364 TCAGAGACCTTCCCGCCGAGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 408
   ::|||
Db 508 GlyAspTrpIrrSerThrIleYrThrAsnCyStrpValIrrpGIYTrpGIYrPheSerLysGIu 527
QY 409 ---GGCAGTGGAGCAGATGATGATGAGCGCCTCCACCCGATTTCTCTGAAAGCAGGTGAAG 465
   |||||
Db 528 LysGIYGIInIleGIInAsn-----IleuGIInLysValAsn 539
QY 466 GTCCCGAATAATGGAAACACACATTTGTGACGAAATAACACCTTGGCGCCTACACGGGA 525
   ::|||
Db 540 IleProLeuValThraShnGIuGIInLysGIInLysArgTYr----- 552
QY 526 GACGACGTCCCGATGCTCCGATGACGACAGTGGTGGTGGGAGACACCCCG-----AGG 579
   |||
Db 553 GlnAspTrpIrrLysIleThrGIIn---ArgMetValLysAlaGIYTrpLYSGIuGIYGIYLys 571
QY 580 GACTCATGCCAGGGGACTCCGAGGGCCCTGTCTGTGCAAGGTGAATGGACACTGGCCTG 639
   |||||
Db 572 AspAlaCySLysGIYAspSerGIYGIYProLeuValCySLysHisAsnGIYMetTrpArg 591
QY 640 CAGGGGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 699
   |||||
Db 592 LeuValGIYIleThrSerTrpGIYGIInLysCysAlaArgGIInProGIYValTYr 611
QY 700 ACCCGTTCACCTACTACTCTGGACTGGATCC 729
   |||||
Db 612 ThrLysValAlaIaGIuTYrMetAspTrpIle 621
```

Search completed: January 31, 2003, 06:59:25
Job time : 33.5 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 05:19:47 ; Search time 62 Seconds
(without alignments)
\$586.825 Million cell updates/sec

Title: US-09-598-982-20
771
Perfect score: 1 gggccctcgagaagaat.....cgtgaagcggccctcgt 771
Sequence: 1 gggccctcgagaagaat.....cgtgaagcggccctcgt 771

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCR_NEM_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726.2	94.2	1081	10	US-09-954-456-2126 Sequence 2126, Ap
2	223.2	28.9	616	10	US-09-954-456-2242 Sequence 2242, Ap
3	201.4	26.1	1110	9	US-10-041-006A-1 Sequence 1, Appli
4	201.4	26.1	1110	12	US-10-040-655-1 Sequence 1, Appli
5	201.4	26.1	1129	9	US-10-028-072-221 Sequence 221, App
6	193.8	25.1	1130	9	US-10-041-006A-8 Sequence 8, Appli
7	193.8	25.1	1130	12	US-10-040-655-8 Sequence 8, Appli
8	191.6	24.9	2847	10	US-09-888-615-35 Sequence 35, Appli
9	187.8	24.4	1613	12	US-10-041-400A-1 Sequence 1, Appli
10	187.8	24.4	1613	12	US-10-041-264A-1 Sequence 1, Appli
11	187.6	24.4	1613	12	US-10-042-091A-1 Sequence 1, Appli
12	187.6	24.3	1122	10	US-09-900-754-1 Sequence 1, Appli
13	184.4	23.9	249	10	US-09-960-352-1410 Sequence 1410, Ap
14	181.2	23.5	1130	12	US-10-041-400A-8 Sequence 8, Appli
15	181.2	23.5	1130	12	US-10-041-264A-8 Sequence 8, Appli
16	181.2	23.5	1130	12	US-10-042-091A-8 Sequence 8, Appli
17	180.4	23.4	714	9	US-10-067-761-9 Sequence 9, Appli
18	180.4	23.4	714	10	US-09-804-156-9 Sequence 9, Appli
19	180	23.3	262	10	US-09-960-352-8091 Sequence 8091, Ap

Result No.	Score	Query Match	Length	ID	Description
20	176.8	22.9	248	10	US-09-960-352-11859 Sequence 11859, A
21	145.8	18.9	867	10	US-09-888-615-56 Sequence 56, Appli
22	140	18.2	1834	10	US-09-948-094-1 Sequence 1, Appli
23	140	18.2	1834	10	US-09-880-107-2214 Sequence 2214, Ap
24	140	18.2	1834	10	US-09-967-768A-141 Sequence 141, App
25	132.4	17.2	1668	10	US-09-925-301-208 Sequence 208, App
26	131.4	17.0	2457	10	US-09-888-615-52 Sequence 52, Appli
27	131.2	17.0	1352	10	US-09-908-711-56 Sequence 56, Appli
28	131.2	17.0	1352	10	US-09-764-898-134 Sequence 134, App
29	131.2	17.0	1352	10	US-09-764-898-135 Sequence 135, App
30	131.2	17.0	1378	9	US-09-905-291A-262 Sequence 262, App
31	131.2	17.0	1378	9	US-09-902-853-262 Sequence 262, App
32	131.2	17.0	1378	9	US-09-907-824-262 Sequence 262, App
33	131.2	17.0	1378	9	US-09-907-841-262 Sequence 262, App
34	131.2	17.0	1378	9	US-09-904-011-262 Sequence 262, App
35	131.2	17.0	1378	10	US-09-909-320-262 Sequence 262, App
36	131.2	17.0	1378	10	US-09-909-088B-262 Sequence 262, App
37	131.2	17.0	1430	9	US-10-040-803-1 Sequence 1, Appli
38	131.2	17.0	1430	10	US-09-764-898-63 Sequence 63, Appli
39	129.2	16.8	1166	9	US-10-040-803-2 Sequence 2, Appli
40	125.8	16.3	3387	10	US-09-888-615-38 Sequence 38, Appli
41	122	15.8	1836	10	US-09-832-197-2 Sequence 2, Appli
42	117	15.2	1082	10	US-09-885-441-19 Sequence 19, Appli
43	117	15.2	1100	9	US-09-905-291A-256 Sequence 256, App
44	117	15.2	1100	9	US-09-902-853-256 Sequence 256, App
45	117	15.2	1100	9	US-09-907-824-256 Sequence 256, App

ALIGNMENTS

RESULT 1
US-09-954-456-2126
; Sequence 2126, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/233, 617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234, 052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234, 923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235, 134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235, 637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235, 638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235, 711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235, 720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235, 840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235, 863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2126
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-456-2126
Query Match 94.2%; Score 726.2; DB 10; Length 1081;
Best Local Similarity 98.3%; Pred. No. 7.4e-162;
Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```

OY 17 GAATGTCGGGGGTGAGGAGGGCCCCAGAGCAAGTGGCCCTGGCAGGTTGAGCCTGAGAG 76
Db 66 GCATGTTGGGGGTGAGGAGGGCCCCAGAGCAAGTGGCCCTGGCAGGTTGAGCCTGAGAG 125
OY 77 TCCAGGGCCCAATYATGATGATGCACTTCTCGGGGGGCTCCCTCATCCAGCCCCAGTGGTGC 136
Db 126 TCCGGGACCACTGATGATGCACTTCTCGGGGGGCTCCCTCATCCAGCCCCAGTGGTGC 185
OY 137 TGACCGCCGGGGGCTGGCTGGGAGCCGGAGCTGAAGATCTGGCCCTCAGGGTGGCAAC 196
Db 186 TGACCGCCGGGGGCTGGCTGGGAGCCGGAGCTGAAGATCTGGCCCTCAGGGTGGCAAC 245
OY 197 TGCGGGAGCAGCAGCTTACTACTACAGCAGCAGCAGCTGCGCGGGTCCAGAGATCATCTGTC 256
Db 246 TGCGGGAGCAGCAGCCTTACTACTACAGCAGCAGCAGCTGCGCGGGTCCAGAGATCATCTGTC 305
OY 257 ACCCAAGTTCACACCCGCCAGATCGAGCGGAGACATCCCTGCTGGAGTGGAGAGC 316
Db 306 ACCCAAGTTCACACCCGCCAGATCGGAGCGGAGACATCCCTGCTGGAGTGGAGAGC 365
OY 317 CGGTGAAGTTCACACCCGCCAGATCGGAGCGGAGACATCCCTGCTGGAGTGGAGAGC 376
Db 366 CGGTGAAGTTCACACCCGCCAGATCGGAGCGGAGACATCCCTGCTGGAGTGGAGAGC 425
OY 377 CCGCGGGGATGCGCTGCTGAGGAGTCCAGTGGCTGGGCGGATGAGACATGATGAGCCCTCC 436
Db 426 CCGCGGGGATGCGCTGCTGAGGAGTCCAGTGGCTGGGCGGATGAGACATGATGAGCCCTCC 485
OY 437 CACCGCCATTTCTCTGAAAGCAGGTGAAGGTCCCATTAATGAGAAAACCAATTTGTGAGC 496
Db 486 CACCGCCATTTCTCTGAAAGCAGGTGAAGGTCCCATTAATGAGAAAACCAATTTGTGAGC 545
OY 497 CAATAATACACTTGGCGGCTACAGGGGAGAGAGCTCCGGATCGTGGTGCAGCATGTC 556
Db 546 CAATAATACACTTGGCGGCTACAGGGGAGAGAGCTCCGGATCGTGGTGCAGCATGTC 605
OY 557 TGTGTCCCGGAAACACCCGGAGGACTCATGTCAGGAGGAGTCCGGAGGAGGAGGAGTGT 616
Db 606 TGTGTCCCGGAAACACCCGGAGGACTCATGTCAGGAGGAGTCCGGAGGAGGAGGAGTGT 665
OY 617 GCAAGGTGATGAGCAGCTGGCTGACAGGGGGGCTGATCGTGGGGCGAGGGCTGTGCC 676
Db 666 GCAAGGTGATGAGCAGCTGGCTGACAGGGGGGCTGATCGTGGGGCGAGGGCTGTGCC 725
OY 677 ACCCAACCGGCTGATCTACACCCGTTGACACCTACTACTGAGATGATGATCCACACT 736
Db 726 ACCCAACCGGCTGATCTACACCCGTTGACACCTACTACTGAGATGATGATCCACACT 785
OY 737 ATGTCCCCAAAAAGCCGTGMAAGCGCC 763
Db 786 ATGTCCCCAAAAAGCCGTGATGATGAGC 812

```

```

; PRIOR APPLICATION NUMBER: US/60/235, 637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235, 638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235, 711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235, 720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235, 840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235, 863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2242
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: n=a, l,g or c
US-09-954-456-2242

Query Match 28.9%; Score 223.2; DB 10; Length 616;
Best Local Similarity 93.5%; Pred. No. 8.2e-44;
Matches 286; Conservative 0; Mismatches 15; Indels 5; Gaps 5;

OY 460 GTGAAGTCCCAATATGAGAAACACACATTTGTGACGGCAAAATCCACTTGGCGCTAC 519
Db 607 GTGAAGTCCCAATATGAGAAACACACATTTGTGACGGCAAAATCCACTTGGCGCTAC 550
OY 520 ACGGAGACAGACTCCGATCGCTCCGTC-ACGACATGCTGTGTGCGGGAGAACCCGGAG 578
Db 549 ACGGAGACAGACTCCGATCGCTCCGTC-ACGACATGCTGTGTGCGGGAGAAC-CCGGAG 491
OY 579 GAGCTCATGCCAGGGCG-ACTCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 637
Db 490 GAGCTCATGCCAGGGCGAAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 431
OY 638 TGCAAGCGGGGGTGTGCAAGCTGGGGGCAAGGGCTGTGCCAGGCCAAAGGGCCCTGGCATCT 697
Db 430 TAGAGGGGGGGTGTGCAAGCTGGGGGCAAGGGCTGTGCCAGGCCAAAGGGCCCTGGCATCT 371
OY 698 ACACCCGTGTACTACTACTACTGATGATGATGATGATGATGATGATGATGATGATGAT 757
Db 370 ACACCCGTGTACTACTACTACTGATGATGATGATGATGATGATGATGATGATGATGAT 311
OY 758 GCGGCC 763
Db 310 TCAGGC 305

```

```

RESULT 3
US-10-041-006A-1
; Sequence 1, Application US/10041006A
; Patent No. US20020168754A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: Protease P
; FILE REFERENCE: ORF-1032
; CURRENT APPLICATION NUMBER: US/10/041.006A
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-041-006A-1

```

Query Match 26.1%; Score 201.4; DB 9; Length 1110;
Best Local Similarity 57.4%; Pred. No. 1.2e-38;
Matches 433; Conservative 0; Mismatches 301; Indels 21; Gaps 3;

12 GAAAGAAATCGTCGGGGGTGCAGAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTAGCCT 71
131 GAACCGAAATGTTGGGGGGGAGAGACACGAGAGAGGGCCGAGTGGCCCTGGCAAGTGCAT 190
72 GAGAGTCCAGGGCCCATATGATGATCTTGGGGGGGCTCCCTCATCCACCCCAAGT 131
191 -----CCAGCCGACGGAAGCCACTTTTCCGGGGGACGCTCATATGCGGAGCATGT 241
132 GGTGCTGACCGCGCGGGCGTGGTGGGACCGGACGTCAGAGATCTGGCC-----GCCCT 185
242 GGTCTGACGGCGTGGCACTGCTCCGCAACAACCTCTGAGACGTCCTCCCTGTACAGGTCT 301
186 CAGGCTGCACTGGCGGAGACAGCCTCTACTACAGACAGCAAGCTCTCCGCTCAGCAG 245
302 GCTGGGGGCAAGGCAAGTGTAGTCCAGCCGGGACCAACGCTATGTATGCCGGGTAGGCA 361
246 GATCATCTGTCACCCACAGATCTTACACCGCCAGATCGGAGGGGAGATCGCCCTGTGGA 305
362 GGTGAGAGCAACCCCTTACAGAGGACAGCCGCTCCAGCCTGACGTGGCCCTGGTGA 421
306 GCTGAGAGACCGGAGTGAAGGTCTCCAGCCGTCACACAGGTCACACCCCTCCCTGCTTC 365
422 GCTGGAGGCAAGTGGCCCTTACCAATATACATCTCCCGTGGTGGCTCCTGACCCCTC 481
366 AGAGACTTCCCGCGGGATGCGCTGCTGCTACTGCTGGGCGAGTGGAGCAATGA 425
482 GGTGATCTTTGAGACGGGAGTGAATGATGCTGCTGCTGGGGGAGCCCAAGTGA 541
426 TGAGACCTTCCCGCGGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
542 AGACTCTCTGCGCGGAGACCGCGGATCTGCAAGAACTCCGCTGTGCTGCTGCTGCTGCT 601
486 CATTGTGTGACGCAAAATACACCTTGGCGCTTACACAGGAGAGACAGCTCCGATGCTCC 545
602 CAAGTCAACCTGCTCTACAGCAAAAGACACCGAGTGTGGCTTACCAAAACCAATCA 661
546 TGACGACATGCTGTGTGCGGG-----GAACACCGGAGAGACTATGCGCAGGGGACTC 599
662 GAATGACATGCTGTGTGCGGGCTTCCAGGAGGAGGCAAGAGTGCCTGCAAGGGGACTC 721
600 CGAGGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
722 GGGCGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
660 GGGCGAGGGCTGTGCGCAGCCCAACCGGCTGGCATCTACACCCGCTGTGACCTACTACTT 719
782 GGGTGTAGGGCTGTGCGCGCAGAACCGCCAGAGTGTCTACATCCGCTGTACCCGCCACCA 841
720 GGACTGTGATCCACACTATGTCGCCCAAAAAGCCGT 754
842 CAACGTGATCCATCGGATCCGCCAAAACCTGCAGT 876

RESULT 4
US-10-040-655-1
; Sequence 1, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

LENGTH: 1110
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-655-1

Query Match 26.1%; Score 201.4; DB 12; Length 1110;
Best Local Similarity 57.4%; Pred. No. 1.2e-38;
Matches 433; Conservative 0; Mismatches 301; Indels 21; Gaps 3;

12 GAAAGAAATCGTCGGGGGTGCAGAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTAGCCT 71
131 GAACCGAAATGTTGGGGGGGAGAGACACGAGAGAGGGCCGAGTGGCCCTGGCAAGTGCAT 190
72 GAGAGTCCAGGGCCCATATGATGATCTTGGGGGGGCTCCCTCATCCACCCCAAGT 131
191 -----CCAGCCGACGGAAGCCACTTTTCCGGGGGACGCTCATATGCGGAGCATGT 241
132 GGTGCTGACCGCGCGGGCGTGGTGGGACCGGACGTCAGAGATCTGGCC-----GCCCT 185
242 GGTCTGACGGCGTGGCACTGCTCCGCAACAACCTCTGAGACGTCCTCCCTGTACAGGTCT 301
186 CAGGCTGCACTGGCGGAGACAGCCTCTACTACAGACAGCAAGCTCTCCGCTCAGCAG 245
302 GCTGGGGGCAAGGCAAGTGTAGTCCAGCCGGGACCAACGCTATGTATGCCGGGTAGGCA 361
246 GATCATCTGTCACCCACAGATCTTACACCGCCAGATCGGAGGGGAGATCGCCCTGTGGA 305
362 GGTGAGAGCAACCCCTTACAGAGGACAGCCGCTCCAGCCTGACGTGGCCCTGGTGA 421
306 GCTGAGAGACCGGAGTGAAGGTCTCCAGCCGTCACACAGGTCACACCCCTCCCTGCTTC 365
422 GCTGGAGGCAAGTGGCCCTTACCAATATACATCTCCCGTGGTGGCTCCTGACCCCTC 481
366 AGAGACTTCCCGCGGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
482 GGTGATCTTTGAGACGGGAGTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
426 TGAGACCTTCCCGCGGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
542 AGACTCTCTGCGCGGAGACCGCGGATCTGCAAGAACTCCGCTGTGCTGCTGCTGCTGCT 601
486 CATTGTGTGACGCAAAATACACCTTGGCGCTTACACAGGAGAGACAGCTCCGATGCTCC 545
602 CAAGTCAACCTGCTCTACAGCAAAAGACACCGAGTGTGGCTTACCAAAACCAATCA 661
546 TGACGACATGCTGTGTGCGGG-----GAACACCGGAGAGACTATGCGCAGGGGACTC 599
662 GAATGACATGCTGTGTGCGGGCTTCCAGGAGGAGGCAAGAGTGCCTGCAAGGGGACTC 721
600 CGAGGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
722 GGGCGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
660 GGGCGAGGGCTGTGCGCAGCCCAACCGGCTGGCATCTACACCCGCTGTGACCTACTACTT 719
782 GGGTGTAGGGCTGTGCGCGCAGAACCGCCAGAGTGTCTACATCCGCTGTACCCGCCACCA 841
720 GGACTGTGATCCACACTATGTCGCCCAAAAAGCCGT 754
842 CAACGTGATCCATCGGATCCGCCAAAACCTGCAGT 876

RESULT 5
US-10-028-072-221
; Sequence 221, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Mei-Qiang

APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang
 TITLE OF INVENTION:
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US//10/028,072
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059836
 PRIOR FILING DATE: 1997-09-24
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062285
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062814
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/062816
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063045
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063082
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/063127
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063327
 PRIOR FILING DATE: 1997-10-27
 PRIOR APPLICATION NUMBER: 60/063329
 PRIOR FILING DATE: 1997-10-27
 PRIOR APPLICATION NUMBER: 60/063550
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063561
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063704
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063733
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063735
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063738
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063755
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064248
 PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/064809
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065846
 PRIOR FILING DATE: 1997-11-17
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/066453
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/066511
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/069212
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069278
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069334
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069694
 PRIOR FILING DATE: 1997-12-16
 PRIOR APPLICATION NUMBER: 60/072320
 PRIOR FILING DATE: 1998-01-23
 PRIOR APPLICATION NUMBER: 60/073612
 PRIOR FILING DATE: 1998-02-04
 PRIOR APPLICATION NUMBER: 60/074086
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: 60/074092
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-02-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081695
 PRIOR FILING DATE: 1998-04-14
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081818
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082999
 PRIOR FILING DATE: 1998-04-24
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085149
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085579

```

? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085704
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/086414
? PRIOR FILING DATE: 1998-05-22
? PRIOR APPLICATION NUMBER: 60/086430
? PRIOR FILING DATE: 1998-05-22
? PRIOR APPLICATION NUMBER: 60/087106
? PRIOR FILING DATE: 1998-05-28
? PRIOR APPLICATION NUMBER: 60/088026
? PRIOR FILING DATE: 1998-06-04
? PRIOR APPLICATION NUMBER: 60/088730
? PRIOR FILING DATE: 1998-06-10
? PRIOR APPLICATION NUMBER: 60/088741
? PRIOR FILING DATE: 1998-06-10
? PRIOR APPLICATION NUMBER: 60/088810
? PRIOR FILING DATE: 1998-06-10
? PRIOR APPLICATION NUMBER: 60/088858
? PRIOR FILING DATE: 19/98-06-11
? PRIOR APPLICATION NUMBER: 60/089532
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089599
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089907
? PRIOR FILING DATE: 1998-06-18
? PRIOR APPLICATION NUMBER: 60/089947
? PRIOR FILING DATE: 1998-06-19
? PRIOR APPLICATION NUMBER: 60/090349
? PRIOR FILING DATE: 1998-06-23
? PRIOR APPLICATION NUMBER: 60/090429
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090445
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090538
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090863
? PRIOR FILING DATE: 1998-06-26
? PRIOR APPLICATION NUMBER: 60/091360
? PRIOR FILING DATE: 1998-07-01
? PRIOR APPLICATION NUMBER: 60/091519
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091982
? PRIOR FILING DATE: 1998-07-07

```

Query Match 26.1%; Score 201.4; DB 9; Length 1129;

Best Local Similarity 57.4%; Pred. No. 1.2e-38;

Matches 433; Conservative 0; Mismatches 301; Indels 21; Gaps 3;

```

QY 12 GAAAGATCGTGGGGGTCAGGAGGCCCCCAAGGAGCAGTGGCCCTGGCAGGTAGCCT 71
DB 131 GAACCAAGTGTGGGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 190
QY 72 GAGAGTCCAGGCGCCACTACTGATGCACTTCTGCGGGGGCTCCCTCATTCCACC 131
DB 191 -----CGAGCGCAAGGAAAGCCACTTGTGCGGGGGGAGCGCTATGCGGAGGAGG 241
QY 132 GGTGTCAGACCGCGCGGCTGCGTGGGAGCCGGAAGTCAAGGATTCGGCC-----GCCCT 185
DB 242 GGTTCCTGAGCGGTGGCCACTGCTTCCGCAACACTCTGTAGAGGTCCCTGTACCAGGTCT 301
QY 186 CAGGGTCAACTGCGGGGAGCAGCAGCCTTACTACTAGCAAGCAAGCAAGCTCTCCG 245
DB 302 GCTGGGGGCAAGGCAAGCTGTGAGCGCGGAGCAGCAGGCTATGTATGCCCGGGTGGGA 361
QY 246 GATCATCTGACCCACAGCTTCTTACACCGCCAGATCGGAGGAGGAGGAGGAGGAGGAGG 305
DB 362 GGTGAGGAGCAACCCCTTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421
QY 306 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 365
DB 422 GCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 481

```

```

QY 366 AGAGACCTTCCCGCGGGGATGCGTGGSTWCACTGGCTGGGGCGATGTGGACAATGA 425
DB 482 GGTGATCTTTGAGAGGGGATGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
QY 426 TGAGCGCCTCCAGCGCCATTTTCTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 485
DB 542 AGACCTTCCCGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
QY 486 CATTTGTGAGCGAANAATACACTTGGGCGCTTACACGGGAGGAGGAGGAGGAGGAGGAGG 545
DB 602 CAAGTCAACCTGCTTACAGGAAAGACCGGAGTTTGGCTTACCAACCAAAACCATCAA 661
QY 546 TCAACACATGCTGTGTGCCG-----GAACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 599
DB 662 GAATGACATGCTGTGTGCCGCGCGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 721
QY 600 CGGAGGCGCGCGTGTGTGTCAGAAAGTGAATGCAACCTGCTGTGACGCGCGCGTGTG 659
DB 722 GCGCGCGCGCGTGTGTGTCAGAAAGTGAATGCAACCTGCTGTGACGCGCGCGTGTG 781
QY 660 GGGCGAGGCTGTGCGCAAGCCCAACCGCGCTGTCATCTACACCGCTGCTACTACT 719
DB 782 GGTGAGGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 841
QY 720 GCACTGATCCACCACTATGTCCCAAAAGCCGT 754
DB 842 CAACTGATCCATCCGATATCTCCCAAACTGCAGT 876

```

RESULT 6

```

US-10-041-006A-8
? Sequence 8, Application US/10041006A
? Patent No. US2002018754A1
? GENERAL INFORMATION:
? APPLICANT: Andrade-Gordon, Patricia
? APPLICANT: Darrow, Andrew
? APPLICANT: Qi, Jian-shen
? TITLE OF INVENTION: DNA encoding the novel human serine
? TITLE OF INVENTION: protease I
? FILE REFERENCE: ORT-1032
? CURRENT APPLICATION NUMBER: US/10/041.006A
? CURRENT FILING DATE: 2002-01-07
? NUMBER OF SEQ ID NOS: 11
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO: 8
? LENGTH: 1130
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
? OTHER INFORMATION: Protease I in a zymogen activation vector
US-10-041-006A-8

```

Query Match 25.1%; Score 193.8; DB 9; Length 1130;

Best Local Similarity 56.7%; Pred. No. 7.5e-37;

Matches 429; Conservative 0; Mismatches 307; Indels 21; Gaps 3;

```

QY 10 GAGAAAAAATGCTGGGGGTCAGAGGCGCCAGGAGCAAGTGGCCCTGCGCAGGTGAGC 69
DB 157 GATGACAAATGCTGGGGGTCATGCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 216
QY 70 CTGAGAGTCCAGCGCCATACTGATGATGCACTTCTGCGGGGGCTCCCTCATCCACC 129
DB 217 AT-----CGAGGCAAGCGAAGCCACTTCTGCGGGGGAGGCTCTTCYCGGAGACG 267
QY 130 TGGGTCGTGACCGCGCGCGCTGCGTGGAGACCGAGCAAGTCAAGATCTG9-----CCGCC 183
DB 268 TGGGTCTTACAGCGCTGCGGACGCTTCCGCAACACTCTGAAAGAGTCCCTGTACCAAGGTC 327
QY 184 CTCAGGCTCAACTGCGGGAGGAGCAGCTTACTTACCAAGCAAGCAGCTGCTGCGGCTCAGC 243
DB 328 CTGCTGGGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 387

```


Matches 370; Conservative 0; Mismatches 234; Indels 18; Gaps 2;

141 GCCTGGGCGGCGTGGGAGCCGAGCAGATCAGATCGCCCGCTCAGAGTGCACACATCGG 200
612 CCCCCGCGGCGGAGAGGAGGAGAGTGGAGCGCTTGGCGTTTAAAGTGCAGAGTGGG 671
201 GGAGCAGCCTTACATACAGAGCAGCAGCTCGCCGCTCAGCAGACATATCGTGCACCC 260
672 GCAGGTGGGCTTATAGAGAGACAGCAGCAGGAGGAGTGGTATCGTCCCGCACCC 731
261 ACAAGTTCACA-----CCGCGCAGATGGAGCCGAGCAATCGCCCTCGTGGAGACTGGA 311
732 CCAAGTACAGCAGAGAGCCTGTGTCCAGGCGGCTGCGGAGCATCGCCCTGATGAACTGGA 791
312 GGAGCGGCTGAAGGTCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 371
792 GCGCCCGGCGGCGCTGT 851
372 CTTCGCGCGGCGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
852 CGTGCCCTCGGGGAAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
432 CCTCCAGCCGCAATTCCTGTGAAAGCAGTGAAGTCCCATATGAAACACATTTTG 491
912 ACTGCTGTGGGCGCCCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
492 TGACGCAAAATATACAC-----CTTGGCGCCTACACGGGAGAGCAGTCCTCCGATCGT 542
972 TAACGAGACCTGT 1031
543 CCGTGCAGCAGATGT 602
1032 CAAGGAGCAGACAGCTGT 1091
603 AGGGCCCTGT 662
1092 GGGCCCTGT 1151
663 CGAGGCTGT 722
1152 CAACTCTGCAGGCGCTTGT 1211
723 CTGATCCAGCAGCATATGTCCCG 744
1212 CTGATCCAGCAGCATATGTCCCG 1233

RESULT 9
US-10-041-400A-1
Sequence 1, Application US/10041400A
Patent No. US20020110895A1
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1613
TYPE: DNA
ORGANISM: Homo sapiens
US-10-041-400A-1

Query Match 24.4%; Score 187.8; DB 12; Length 1613;
Best Local Similarity 36.9%; Pred. No. 2.1e-35;
Matches 414; Conservative 0; Mismatches 292; Indels 21; Gaps 3;

17 GAATCGTGGGGGTGAGAGGGCCCGCAGAGCAAGTGGCCCTGGCAGGAGTGCAGAG 76
175 GGATCGTGGGGGCGCGGATGATGCGCGAGCAGAGTGGCCCTGGGAGGCGAGCATCCAGC 234
77 TCCAGCGCCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 136
235 ATCCGAGGGCA-----CACGHTGTGGGGGCTGCTATCCAGTCCCGCCAGTGGGTGC 285
137 TGACCGCGGCGCGCTGCTGGAGCCGAGCAGTCAAG-----GATCGGCCCGCCCTCAGGG 190
286 TGACAGCGGGGACTGCTTCCCGCAGAGGAGCATGCGCAGCTGAGTACCGCGGTGCGCTGG 345
191 TGCAACTGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 250
346 GGGCGCTGCTGTGGGCTTCACACTGCCCCCGACGCTCTCGGTGCGGTGGAGGGGTGC 405
231 TCGTGCACCCACAGTGTACACCGCCAGANTCGAGCGGACATGCGCTGTGTGAGACTGG 310
406 TGCTGCCCCGACTACTCCAGAGACGGGGCCCCCGGGGAGCAGCAGTGCCTGCTGAGCTGC 465
311 AGAGCCCGGTGAAGTCTTCCAGCCACGTCACACGCTACCGCTGCCCCCTGCTCAGAGA 370
466 GTGCGCCGCGGCTGAGCCCTGAGCCCTGCTGCAACCCGCTGCTGCTGCTGCTGCTGCTG 525
371 CTTTCCCGCGGAGTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
526 GCGCGCCGCGGCGCACACCATGCGCGGCTGCACCGGCTGTGGGGACGCTCCGCGCAGAGATGC 585
431 GCGTCCACCCGCAATTCCTGTGAAAGCAGTGTGAAAGTGTCCCATATGAAACACATTTT 490
586 CCGCTCAGAGTGGGAGACCGGTACAAAGAGTAAAGGTGTCGCGGTGAGTCCAGCAGCT 645
491 GTGAGCGCAAAATATACACCTTGGCGGCTTACAGGAGAGAGAGTCCGCTGCTGAGC 550
646 GCGAGGCGCTTACACCGCTGCGGCGGAGGCTGCCAGGCTGAGGAGGCTTGTGCTGCTG 705
551 ACATGCTGTGGCCGAAACACCCGG-----AGGACTCAATGAGGGCGACGCTCCGAG 604
706 GAGTCTGT 765
605 GCGCCCTGT 664
766 GACCTGTGACCTGCCTGCAAGT 825
665 AGGCTGT 724
826 AGGTTGT 785
725 GGATCCA 731
886 GGATTTCA 892

RESULT 10
US-10-041-264A-1
Sequence 1, Application US/10041264A
Patent No. US20020142446A1
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,264A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1613

TYPE: DNA
ORGANISM: Homo sapiens
US-10-041-264A-1

Query Match
Best Local Similarity 56.9%; Score 187.8; DB 12; Length 1613;
Matches 414; Conservative 0; Mismatches 292; Indels 21; Gaps 3;

17 GAATGCTGGGGGATGACAGAGGCCCCCAGAGCAAGTGGCCCGGAGGTGAGCCCGAGAG 76
175 GGATGCTGGGGGATGACAGAGGCCCCCAGAGCAAGTGGCCCGGAGGTGAGCCCGAGAG 234
77 TCACAGGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
235 ATCTGGGGGCA-----CACGTGTGCGGGGGGTGCTCATATGCCCCCAGTGGGGTGC 285
137 TGACCGCCCGGCGGTGCTGGAGCCGGACGTCAG-----GATCTGGCCCGCCCTCAGGG 190
286 TGACAGCGCCGACACTGCTTCCCAAGAGGACATGCTGATGATGATGATGATGATGATGAT 345
191 TGCAACTGCGGGAGGACGACCTTACTACTACTACTACTACTACTACTACTACTACTACTACT 250
346 GGGCGCTGCTGTGTGGGCTTCCACTACTACTACTACTACTACTACTACTACTACTACTACT 405
251 TGTGTGACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 310
406 TGTGTGACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 465
311 AGGAGCCGGTGAAGTCTTCCAGCCACGTCACACGCTACACCTGCCCCCTGCTCAGAGA 370
466 GTGCGCCCGGTGCTGCTGAGCCGCTGCGCTCAACCCGCTGCTGCTGCTGCTGCTGCTGCTG 525
371 CCTTCCCCGGGGGATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
526 GCCCGCCCGCGGACACACATGCGGGGTCCACCGGCTGAGGGGACGCTCCGCCAGAGAGTGC 585
431 GCTTCCACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 490
586 CCTTCCACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 645
491 GTGAGCAAAAATPACCACCTTGGCGCTTACACGGAAGATGCGAGCGAGCTCCGCTCAGAG 550
646 GCGAGGCGCTTACACACCTTGGCGCTTACACGGAAGATGCGAGCGAGCTCCGCTCAGAG 705
551 ACATGCTGTGTGCGGGGAAACACCGG-----AGGACTCATGACGAGCGGACCTCCGGAG 604
706 GGAATGCTGTGTGCGGGGAAACACCGG-----AGGACTCATGACGAGCGGACCTCCGGAG 765
605 GCGCCCTGGTGTGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
766 GACCTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 825
665 AGGGGTGTGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 724
826 AGGGGTGTGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 885
QY 725 GGATCCA 731
DB 886 GGATTTCA 892

RESULT 11
US-10-042-091A-1
Sequence 1, Application US/10042091A
Patent No. US20020142447A1
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/042.091A

CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1613
TYPE: DNA
ORGANISM: Homo sapiens
US-10-042-091A-1

Query Match
Best Local Similarity 56.9%; Score 187.8; DB 12; Length 1613;
Matches 414; Conservative 0; Mismatches 292; Indels 21; Gaps 3;

17 GAATGCTGGGGGATGACAGAGGCCCCCAGAGCAAGTGGCCCGGAGGTGAGCCCGAGAG 76
175 GGATGCTGGGGGATGACAGAGGCCCCCAGAGCAAGTGGCCCGGAGGTGAGCCCGAGAG 234
77 TCACAGGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
235 ATCTGGGGGCA-----CACGTGTGCGGGGGGTGCTCATATGCCCCCAGTGGGGTGC 285
137 TGACCGCCCGGCGGTGCTGGAGCCGGACGTCAG-----GATCTGGCCCGCCCTCAGGG 190
286 TGACAGCGCCGACACTGCTTCCCAAGAGGACATGCTGATGATGATGATGATGATGATGATGAT 345
191 TGCAACTGCGGGAGGACGACCTTACTACTACTACTACTACTACTACTACTACTACTACTACT 250
346 GGGCGCTGCTGTGTGGGCTTCCACTACTACTACTACTACTACTACTACTACTACTACTACT 405
251 TGTGTGACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 310
406 TGTGTGACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 465
311 AGGAGCCGGTGAAGTCTTCCAGCCACGTCACACGCTACACCTGCCCCCTGCTCAGAGA 370
466 GTGCGCCCGGTGCTGCTGAGCCGCTGCGCTCAACCCGCTGCTGCTGCTGCTGCTGCTGCTG 525
371 CCTTCCCCGGGGGATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
526 GCCCGCCCGCGGACACACATGCGGGGTCCACCGGCTGAGGGGACGCTCCGCCAGAGAGTGC 585
431 GCTTCCACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 490
586 CCTTCCACACCAAGTTTCTACACACCGCCAGATGCGAGCGAGATGCGCCCTGCTGAGACTGG 645
491 GTGAGCAAAAATPACCACCTTGGCGCTTACACGGAAGATGCGAGCGAGCTCCGCTCAGAG 550
646 GCGAGGCGCTTACACACCTTGGCGCTTACACGGAAGATGCGAGCGAGCTCCGCTCAGAG 705
551 ACATGCTGTGTGCGGGGAAACACCGG-----AGGACTCATGACGAGCGGACCTCCGGAG 604
706 GGAATGCTGTGTGCGGGGAAACACCGG-----AGGACTCATGACGAGCGGACCTCCGGAG 765
605 GCGCCCTGGTGTGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
766 GACCTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 825
665 AGGGGTGTGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 724
826 AGGGGTGTGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 885
QY 725 GGATCCA 731
DB 886 GGATTTCA 892

RESULT 12
US-09-900-754-1
Sequence 1, Application US/09900754
Patent No. US20020026554A1
GENERAL INFORMATION:


```

; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING TRYPTASE GENE
; TITLE OF INVENTION: DISRUPTIONS
; FILE REFERENCE: R-372
; CURRENT APPLICATION NUMBER: US/09/900,754
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/216,109
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US 60/223,172
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/244,111
; PRIOR FILING DATE: 2000-10-26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-900-754-1

```

```

Query Match          24.3%; Score 187.6; DB 10; Length 1122;
Best Local Similarity 58.9%; Pred. No. 2,1e-35;
Matches 432; Conservative 0; Mismatches 269; Indels 33; Gaps 5;

```

```

OY 17 GAATGCTCGGGGTCAGAGCCGCCAGGAGCAAGTGGCCCTGACAGTGGAGGAG 76
DB 86 GAATGCTGGGAGGAGGATGCTGCCAGGAGCAATGGCCGTGGAGGCTAGCT----- 140
OY 77 FCCAGGCCCCAATCTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCAGTGGTGC 136
DB 141 ----CCGTGTGCAAGAGTGCACGTGTGTGGAGGCTCCCTGCTCACTGATGAGATGGTGC 196
OY 137 TGACCGCGCGGGGTCGCGGGGAGACCGSAGATGATGGCCGCCCTCAGSAGTCAAC 196
DB 197 TCAACAGCAACCCACTGCTCTCTGGGTCTGTGAATC-----GTCTGATTAACAGTGCAC 253
OY 197 TCGCGGAGGAGGACCTCTACTACAGACCAAGCTCTGCCGGTCAAGAGATCATGTCG 256
DB 254 TGGAGAGGCTTAAAGGTCACACATGTCTGCCACTCTCCACTGTAAAGAGATCATATGT 313
OY 257 ACCCAGACTTTCAC--ACCGCCAGATGGAGCGGACATCCGCCCTGTGGAGCTGGAAG 313
DB 314 ACACCTGGCTCTCCAGGACCCCGGGGTCCAGTGGGACATTTGCCCTGTGCAAGCTGTCC 373
OY 314 AGCCGGTGAAGGCTCCAGCAAGTCCACAGSGTCAACCCCGCCCTGGCTCAGAACCT 373
DB 374 CCCCCTGGCCCTTTCAGACAGGTCACGCTGTGTGCTCCAGAGGCTCAGCTGACT 433
OY 374 TCCCCCGGGGATGCGCTGTGCTGCTGCTGCTGGGGGATGGAGCAATGATGAGCGCC 433
DB 434 TCTACCTGTGGATGGAGTGTGCTGTGCTGCTGGGTGCTGCTGCTGCTGCTGCTGCTG 493
OY 434 TCCACCGCCCAATCTCTGTAAGACAGGTGAAGTCCCAATATGAAACACCATTTGTG 493
DB 494 TGAAGCCCCCAACAACCTTTCAGAGGCCCAAAAGTCTCTGTGGTGGAT----- 540
OY 494 AGCGAAATATACCACTTGGGCTTACAGGGAGACAGTCCGCAATGCTCCCTGTGAGACA 553
DB 541 --GTAAGACTTGCAGACCAAGCTTACAAATATGTCACATGACACCTTCATCCAGCA 598
OY 554 TGTGTGTCCCGGGAACACCCGGAGGACTCATGCCAGGGCCATCCGGAGGGCCCTGTG 613
DB 599 TGTATATGGCCCGGGGGCCCTG---GGGATGCTCCAGGATGACTCTGTGAGGGCCACTG 655
OY 614 TGTGCAAGTGAATGGCACTGCTGCAAGCGGAGGCTGTGCTCACTGCTGGCGGAGGCTGTG 673
DB 656 TCTGCCAGGTGGCTGGAACCTTGCAGACCGCCGCTTGTCACTGGGTGGAGGCTGTG 715
OY 674 CCGAGCCAAACCGGCTGATCTACACCGGCTCACTACTGCTGAGTGGATCCAC 733
DB 716 GCGCGCTGACCGCCCTGGGCTGTATGCGCGGGGTACTGCTATGTAATGAACTGATCCAC 775

```

```

OY 734 ACTANGTCCCAAA 747
DB 776 ACCACATCCCGAA 789

```

```

RESULT 13
US-09-960-352-1410/C
; Sequence 1410, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengding
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1410
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 07-LIB188-011-Q1-E1-B11
; US-09-960-352-1410

```

```

Query Match          23.9%; Score 184.4; DB 10; Length 249;
Best Local Similarity 85.1%; Pred. No. 8.7e-35;
Matches 206; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```

```

OY 503 ACCACCTTGGCGCTACAGCGGAGACGATCCCGCATCGTCCGTGACAGCATGTGTG 562
DB 249 ACCACTCTGGCCCTGCTCCACGGGGGACACGCTCCCATCTGTCGGAGGACATGCTGTG 190
OY 563 CCGGGAACCCCGGAGGACTATGCCAGGGGACATCCCGAGGGCCCTGTGTGCAAG 622
DB 189 CTGGGAGACAGCGGGAGGAACTCTGCCAGGGGACTCTGAGAGGGCCCTGATGCAAG 130
OY 623 TGAATGGACCTGGCTGACAGGGGGGCTGTGATGCTGGGGCCAGGGCTGTGCCAC 682
DB 129 TGAATGGACCTGGCTGACAGGGGGGCTGTGATGCTGGGGCCAGTGTGCGGAAC 70
OY 683 ACCGGCTGGCATCTACACCCTGTCACCTACTACTTGGACTGTGATCCACCACTATG 742
DB 69 ACCGGCCCGCATCTACACCCTGTCACCTCTACTTGGACTGTGATCCAGCCGTATCC 10
OY 743 CC 744
DB 9 CC 8

```

```

RESULT 14
US-10-041-400A-8
; Sequence 8, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Q1, Jensen
; TITLE OF INVENTION: DNA Encoding the Human Serine
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/10/041,400A
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US/09/387,375
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Artificial sequence

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-8

```

```

Query Match          23.5%; Score 181.2; DB 12; Length 1130;
Best Local Similarity 56.3%; Pred. No. 6.8e-34;
Matches 386; Conservative 0; Mismatches 288; Indels 12; Gaps 2;

```

```

QY 92 GGATGCACTTTCGGGGGGCTCCCTCCATCCACCCCAAGTGGGGTGCACCGCGGGCGGT 151
DB 230 GGGCACACGCTGTGGGGGGTGCCTCATCCGCCCCCAAGTGGGGTGCACAGCGGGCCACT 289
QY 152 GCGTGGGACCCGGACGTCAG-----GATCTGGCCGCCCTCAGGGTGCACACTGGCGGACC 205
DB 290 GCTTCCCAAGAGGGGACATGCCAGCTGAGTACCCGCTGGGGCTGGGGGGGGCTGCTGG 349
QY 206 AGCACCCTTACTACCAAGAACAGCTGCTGCCGGTCCAGAGATCATCTGCACCCACAGT 265
DB 350 GCTCCACCTCGCCGCCACAGCTCTCCGCTCCCGTGGCGAGGGGGTCTGCCCCGGACT 409
QY 266 TCTACACCGCCCAAGATCCGAGGGGAGATCCCTGCTGGAGCTGGAGAGCGGGTGAAG 325
DB 410 ACTCCAGAGACGGGGGCCCGGGGACCTGGCACTGCTGCAAGCTGGCGCGGTGCCGCC 469
QY 326 TCTCCAGCCAGCTCCACAGGTCACCCCTGCCCTCCAGAGACCTTCCCGCCGGGA 385
DB 470 TGAAGCGCTGGCGGCAACCGCTGTGCTGCTCCCGTGGCGGGCGCCGGCCGGCGGGA 529
QY 386 TGGCGTGTGGTCTACTGCTGGGGGGGAGTGGACAAATGATGAGCGCCCTCCACCGCCAT 445
DB 530 CACCAATGCGGGGTCAACCGCTGGGGGGAGCCCTCCGCAAGAGTGGCCCTCCAGAGTGGC 589
QY 446 TTCCTCTGAAGCAGTGAAGGTCCCAATATGGAAGAAACCAATTTGTGACGGCAAAATACC 505
DB 590 GACCGCTAAGAGAGTAAAGGTGCGCTGTGACTGCGGACCTCCGAGCGGCTTACC 649
QY 506 ACCTTGGCCCTACACAGGGGAGAGACGCTCCGATCTCCCGTCCGTCAGCATCTGTGCCG 565
DB 650 ACGTGGGGCGGAGCGTGGCCCCAGGCTGAGCGCATTTGTGCTGGGAGTCTGTGTGCCG 709
QY 566 GGAACACCCGGAG-----GACTCATGCCCAGGGGCGACTCCGGAGGGCCCTGTGTGCA 619
DB 710 GCTAACCCCAAGGGCCCAAGAGAGCGCTGCCAGGATTTCTGGGGGACCTCTGTACCTGCC 769
QY 620 AAGTGAATGGCACTGGCTGCAAGGGGGGGTGTGAGCTGGGGGGAGGGGTGTGGCCAGC 679
DB 770 TGCAGTCTGGAGAGCTGGTCTGTGGTGGGGGTGTGAGCTGGGGCAAGGGTTGTGCCCTGC 829
QY 680 CCAACCGGCTGGCATCTACACCCCGTGCACCTTACTTGGACTGGATTCACCACTATG 739
DB 830 CCAACCGTCCAGGGGCTTACACCAAGTGTGGCCACATATAGCCCTGGATTCAGGGCTCGGG 889
QY 740 TCCCAAAAAAGCCGTGAAGCGGGCCG 765
DB 890 TCACTTCTAATGCTTCTAGATACCCC 915

```

```

RESULT 15
US-10-041-264A-8
; Sequence 8, Application US/10041264A
; Patent No. US20020142446A1
; GENERAL INFORMATION:
; APPLICANT: Barrrow, Andrew
; APPLICANT: Andrade-gordon, Patricia
; APPLICANT: Qi, Jenson
; TITLE OF INVENTION: DNA Encoding the Human Serine
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/10/041,264A
; CURRENT FILING DATE: 2002-01-08
; PRIORITY APPLICATION NUMBER: US/09/387,375
; PRIOR FILING DATE: 1999-08-31

```

```

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-264A-8

```

```

Query Match          23.5%; Score 181.2; DB 12; Length 1130;
Best Local Similarity 56.3%; Pred. No. 6.8e-34;
Matches 386; Conservative 0; Mismatches 288; Indels 12; Gaps 2;

```

```

QY 92 GGATGCACTTTCGGGGGGCTCCCTCCATCCACCCCAAGTGGGGTGCACCGCGGGCGGT 151
DB 230 GGGCACACGCTGTGGGGGGTGCCTCATCCGCCCCCAAGTGGGGTGCACAGCGGGCCACT 289
QY 152 GCGTGGGACCCGGACGTCAG-----GATCTGGCCGCCCTCAGGGTGCACACTGGCGGACC 205
DB 290 GCTTCCCAAGAGGGGACATGCCAGCTGAGTACCCGCTGGGGCTGGGGGGGGCTGCTGG 349
QY 206 AGCACCCTTACTACCAAGAACAGCTGCTGCCGGTCCAGAGATCATCTGCACCCACAGT 265
DB 350 GCTCCACCTCGCCGCCACAGCTCTCCGCTCCCGTGGCGAGGGGGTCTGCCCCGGACT 409
QY 266 TCTACACCGCCCAAGATCCGAGGGGAGATCCCTGCTGGAGCTGGAGAGCGGGTGAAG 325
DB 410 ACTCCAGAGACGGGGGCCCGGGGACCTGGCACTGCTGCAAGCTGGCGCGGTGCCGCC 469
QY 326 TCTCCAGCCAGCTCCACAGGTCACCCCTGCCCTCCAGAGACCTTCCCGCCGGGA 385
DB 470 TGAAGCGCTGGCGGCAACCGCTGTGCTGCTCCCGTGGCGGGCGCCGGCCGGCGGGA 529
QY 386 TGGCGTGTGGTCTACTGCTGGGGGGGAGTGGACAAATGATGAGCGCCCTCCACCGCCAT 445
DB 530 CACCAATGCGGGGTCAACCGCTGGGGGGAGCCCTCCGCAAGAGTGGCCCTCCAGAGTGGC 589
QY 446 TTCCTCTGAAGCAGTGAAGGTCCCAATATGGAAGAAACCAATTTGTGACGGCAAAATACC 505
DB 590 GACCGCTAAGAGAGTAAAGGTGCGCTGTGACTGCGGACCTCCGAGCGGCTTACC 649
QY 506 ACCTTGGCCCTACACAGGGGAGAGACGCTCCGATCTCCCGTCCGTCAGCATCTGTGCCG 565
DB 650 ACGTGGGGCGGAGCGTGGCCCCAGGCTGAGCGCATTTGTGCTGGGAGTCTGTGTGCCG 709
QY 566 GGAACACCCGGAG-----GACTCATGCCCAGGGGCGACTCCGGAGGGCCCTGTGTGCA 619
DB 710 GCTAACCCCAAGGGCCCAAGAGAGCGCTGCCAGGATTTCTGGGGGACCTCTGTACCTGCC 769
QY 620 AAGTGAATGGCACTGGCTGCAAGGGGGGGTGTGAGCTGGGGGGAGGGGTGTGGCCAGC 679
DB 770 TGCAGTCTGGAGAGCTGGTCTGTGGTGGGGGTGTGAGCTGGGGCAAGGGTTGTGCCCTGC 829
QY 680 CCAACCGGCTGGCATCTACACCCCGTGCACCTTACTTGGACTGGATTCACCACTATG 739
DB 830 CCAACCGTCCAGGGGCTTACACCAAGTGTGGCCACATATAGCCCTGGATTCAGGGCTCGGG 889
QY 740 TCCCAAAAAAGCCGTGAAGCGGGCCG 765
DB 890 TCACTTCTAATGCTTCTAGATACCCC 915

```

```

Search completed: January 31, 2003, 06:51:17
Job time : 80 secs

```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 03:51:33 : Search time 56 seconds
(without alignments)
4222.282 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 1 99gcccctcgagaagaat.....cgtgaagcggccgcctcgt 771

Sequence: 1 99gcccctcgagaagaat.....cgtgaagcggccgcctcgt 771

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PC705.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	764.6	99.2	771	US-09-079-970A-4	Sequence 4, Appl
2	731	94.8	1128	US-09-016-366A-20	Sequence 20, Appl
3	731	94.8	1128	US-08-978-404B-15	Sequence 15, Appl
4	731	94.8	1137	US-09-016-366A-18	Sequence 18, Appl
5	731	94.8	1137	US-08-978-404B-13	Sequence 13, Appl
6	728.6	94.5	735	US-09-079-970A-1	Sequence 1, Appl
7	728.2	94.2	1081	US-09-016-366A-22	Sequence 22, Appl
8	726.2	94.2	1081	US-08-978-404B-17	Sequence 17, Appl
9	686.2	89.0	1154	US-09-016-366A-16	Sequence 16, Appl
10	686.2	89.0	1154	US-08-978-404B-11	Sequence 11, Appl
11	477.2	61.9	1219	US-08-978-404B-7	Sequence 7, Appl
12	469.6	60.9	1108	US-09-016-366A-14	Sequence 14, Appl
13	469.6	60.9	1108	US-08-978-404B-20	Sequence 20, Appl
14	463	60.1	1031	US-08-978-404B-1	Sequence 1, Appl
15	445.6	57.8	1103	US-09-016-366A-24	Sequence 24, Appl
16	444	57.6	1097	US-08-978-404B-4	Sequence 4, Appl
17	444	57.6	1097	US-08-845-998-3	Sequence 3, Appl
18	371	48.1	2259	US-09-206-537-3	Sequence 3, Appl
19	371	48.1	2259	US-09-430-854-3	Sequence 3, Appl
20	369.4	47.9	2218	US-08-845-998-5	Sequence 5, Appl
21	369.4	47.9	2218	US-09-206-537-5	Sequence 5, Appl
22	369.4	47.9	2218	US-09-430-854-5	Sequence 5, Appl
23	271.8	35.3	1095	US-08-978-404B-9	Sequence 9, Appl
24	201.4	26.1	1110	US-09-386-653A-1	Sequence 1, Appl
25	193.8	25.1	1130	US-09-386-653A-8	Sequence 8, Appl
26	153	19.8	3757	US-09-016-366A-13	Sequence 13, Appl
27	153	19.8	3757	US-08-978-404B-19	Sequence 19, Appl

28	143.8	18.7	2397	US-08-978-404B-2	Sequence 2, Appl
29	140.6	18.2	1142	US-09-386-642-8	Sequence 8, Appl
30	140.6	18.2	1169	US-09-386-642-7	Sequence 7, Appl
31	131.2	17.0	1430	US-09-386-629-1	Sequence 1, Appl
32	129.2	16.8	1166	US-09-386-629-2	Sequence 2, Appl
33	115.4	15.0	1081	US-09-008-271A-15	Sequence 15, Appl
34	115.4	15.0	1103	US-09-386-642-59	Sequence 59, Appl
35	112.8	14.6	2413	US-09-518-046-1	Sequence 1, Appl
36	108.6	14.1	1109	US-09-088-651-6	Sequence 6, Appl
37	107.6	14.0	1109	US-09-088-651-1	Sequence 1, Appl
38	103.6	13.4	1386	US-08-756-506-3	Sequence 3, Appl
39	103.6	13.4	1755	5225537-1	Patent No. 5225537
40	102.8	13.3	2416	US-09-280-116-57	Sequence 57, Appl
41	100.8	13.1	654	US-09-280-116-57	Sequence 57, Appl
42	98.4	12.8	2544	US-09-518-046-3	Sequence 3, Appl
43	95.6	12.4	1155	US-09-163-951-15	Sequence 15, Appl
44	95.6	12.4	1240	US-09-163-951-14	Sequence 14, Appl
45	94.2	12.2	1387	5270178-1	Patent No. 5270178

ALIGNMENTS

RESULT 1
US-09-079-970A-4
Sequence 4, Application US/090799970A
Patent No. 6274366
GENERAL INFORMATION:
APPLICANT: Mafilt, Mark A.
APPLICANT: Miles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
BETA-TRYPTASE and Method of Making Same
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 970A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 7..753
FEATURE:
NAME/KEY: misc_signal

LOCATION: 7.18
US-09-079-970A-4

Query Match 99.2%; Score 764.6; DB 4; Length 771;
Best Local Similarity 99.3%; Pred. No. 1,4e-164;
Matches 767; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1 GGGCCCCCTCGAGAAAAAATCTGGGGGGTTCAGAGAGCCGCCAGAGACAAAGTCCCTGG 60
1 GGGCCCCCTCGAGAAAAAATCTGGGGGGTTCAGAGAGCCGCCAGAGACAAAGTCCCTGG 60
61 CAGGTGAGCCCTGAGAGTCCAGCCGCCAATCTGATGCACTTCTCCGGGGGCTCCCTCATC 120
61 CAGGTGAGCCCTGAGAGTCCAGCCGCCAATCTGATGCACTTCTCCGGGGGCTCCCTCATC 120
121 CACCCCTCAGTGGGTCTGACCCGCCGGGGTGGGAGCCGGAGCTCAAGATCTGGCC 180
121 CACCCCTCAGTGGGTCTGACCCGCCGGGGTGGGAGCCGGAGCTCAAGATCTGGCC 180
181 GCCCTCAGGGGTCAACTGCGGGGAGCAGCACTCTACTACAGCAGCCAGCTGCTCCCGGTC 240
181 GCCCTCAGGGGTCAACTGCGGGGAGCAGCACTCTACTACAGCAGCCAGCTGCTCCCGGTC 240
241 AGCAGAGATCAGTGTGACCCAGAGTCTACACCCGCCAGATCGGAGCGGACATCCGCCCTG 300
241 AGCAGAGATCAGTGTGACCCAGAGTCTACACCCGCCAGATCGGAGCGGACATCCGCCCTG 300
301 CTGGAGCTGGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACAGGCTCAACCCCT 360
301 CTGGAGCTGGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACAGGCTCAACCCCT 360
361 GCCTGAGAGACCTTCCCGCCGGGAGTCCGCTGCTGCTGCTGCTGGGGGAGTGTGAC 420
361 GCCTGAGAGACCTTCCCGCCGGGAGTCCGCTGCTGCTGCTGCTGGGGGAGTGTGAC 420
421 AATGATGAGCCCTCCACCAGCCATTTCTCTGAAAGCAAGTGAAGTCCCATTAATGAA 480
421 AATGATGAGCCCTCCACCAGCCATTTCTCTGAAAGCAAGTGAAGTCCCATTAATGAA 480
481 AACCCATTTTGTGAGCAAAATACCACTTGGCCCTACAGCGGAGAGACAGCTCCGCATC 540
481 AACCCATTTTGTGAGCAAAATACCACTTGGCCCTACAGCGGAGAGACAGCTCCGCATC 540
541 GTCCTGAGCAGATGCTGTGTGCCGGGAAACACCCGGAGGAGACTCATGCCAGGGCCATCC 600
541 GTCCTGAGCAGATGCTGTGTGCCGGGAAACACCCGGAGGAGACTCATGCCAGGGCCATCC 600
601 GGAGGGCCCTGTGTGTGCAAGGTGAATGGCACTGGCTGCAAGCGGGCGTGTCAAGCTGG 660
601 GGAGGGCCCTGTGTGTGCAAGGTGAATGGCACTGGCTGCAAGCGGGCGTGTCAAGCTGG 660
661 GGGGGGGGCTGAGCCAGCCCAAGCGGGCTGGCATCTACCCCGTGTCACTCACTCACTTTG 720
661 GGGGGGGGCTGAGCCAGCCCAAGCGGGCTGGCATCTACCCCGTGTGTCACTCACTCACTTTG 720
721 GACTGATCCACCACTATGTCCCAAAAAAGCCGTGAAGGGCGCCGCTGT 771
721 GACTGATCCACCACTATGTCCCAAAAAAGCCGTGAAGGGCGCCGCTGT 771

RESULT 2
US-09-016-366A-20
Sequence 20, Application US/09016366A
Patent No. 5955431

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue

CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/016,366A
APPLICATION NUMBER: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-016-366A-20

Query Match 94.8%; Score 731; DB 2; Length 1128;
Best Local Similarity 98.7%; Pred. No. 6e-157;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

17 GAATGTCGGGGGTCAGAGAGCCGCCAGAGCAATGGCCCTGGCAGGTTGAGAG 76
17 GAATGTCGGGGGTCAGAGAGCCGCCAGAGCAATGGCCCTGGCAGGTTGAGAG 76
87 GCATGTTGGGGGTGAGAGAGCCGCCAGAGCAATGGCCCTGGCAGGTTGAGAG 146
87 GCATGTTGGGGGTGAGAGAGCCGCCAGAGCAATGGCCCTGGCAGGTTGAGAG 146
147 TCCAGGCCCATATGATGATGACACTTCTGGGGGCTCCCTCATCCACCCAGTGGGTC 206
147 TCCAGGCCCATATGATGATGACACTTCTGGGGGCTCCCTCATCCACCCAGTGGGTC 206
137 TGACCGCCGGCGTGGTGGAGCCGAGCTCAAGATCTGGCCCTCAAGGTTGCAAC 196
137 TGACCGCCGGCGTGGTGGAGCCGAGCTCAAGATCTGGCCCTCAAGGTTGCAAC 196
207 TGACCGCAGCGACTGCGTGGGAGCCGAGCTCAAGATCTGGCCCTCAAGGTTGCAAC 266
207 TGACCGCAGCGACTGCGTGGGAGCCGAGCTCAAGATCTGGCCCTCAAGGTTGCAAC 266
197 TGCGGAGCAGCAGCTCTACTACTACAGAGCAGCTGCTGCTGAGCAGATCTGTC 256
197 TGCGGAGCAGCAGCTCTACTACTACAGAGCAGCTGCTGCTGAGCAGATCTGTC 256
267 TCGGGAGCAGCAGCTCTACTACTACAGAGCAGCTGCTGCTGAGCAGATCTGTC 326
267 TCGGGAGCAGCAGCTCTACTACTACAGAGCAGCTGCTGCTGAGCAGATCTGTC 326
257 ACCCAGCTTCTACACCCGCCAGATCGGAGCGGACATCGCCCTGTGAGCTGAGAGC 316
257 ACCCAGCTTCTACACCCGCCAGATCGGAGCGGACATCGCCCTGTGAGCTGAGAGC 316
327 ACCCAGCTTCTACACCCGCCAGATCGGAGCGGACATCGCCCTGTGAGCTGAGAGC 386
327 ACCCAGCTTCTACACCCGCCAGATCGGAGCGGACATCGCCCTGTGAGCTGAGAGC 386
317 CGGTGAAGTCTCCAGCCAGCTCCACACAGGTGACCTGCTGCTGAGCAGATCTGTC 376
317 CGGTGAAGTCTCCAGCCAGCTCCACACAGGTGACCTGCTGCTGAGCAGATCTGTC 376
387 CGGTGAAGTCTCCAGCCAGCTCCACACAGGTGACCTGCTGCTGAGCAGATCTGTC 446
387 CGGTGAAGTCTCCAGCCAGCTCCACACAGGTGACCTGCTGCTGAGCAGATCTGTC 446
377 CCGCGGGGATGCGTGGGTGATGCTGGGCGGATGGGAGCAATGATGAGGCGCTCC 436
377 CCGCGGGGATGCGTGGGTGATGCTGGGCGGATGGGAGCAATGATGAGGCGCTCC 436
447 CCGCGGGGATGCGTGGGTGATGCTGGGCGGATGGGAGCAATGATGAGGCGCTCC 506
447 CCGCGGGGATGCGTGGGTGATGCTGGGCGGATGGGAGCAATGATGAGGCGCTCC 506
437 CACCCCATTTCTCTGAGAGCAGTGAAGGTCCCAATGAGAAAAACCAATTTTGTGAGC 496
437 CACCCCATTTCTCTGAGAGCAGTGAAGGTCCCAATGAGAAAAACCAATTTTGTGAGC 496
507 CACCCCATTTCTCTGAGAGCAGTGAAGGTCCCAATGAGAAAAACCAATTTTGTGAGC 566
507 CACCCCATTTCTCTGAGAGCAGTGAAGGTCCCAATGAGAAAAACCAATTTTGTGAGC 566
497 CAAAATFACCACTTGGGCTTACAGAGGAGAGCAGTCCGATGCTGCTGAGCAGATTC 556
497 CAAAATFACCACTTGGGCTTACAGAGGAGAGCAGTCCGATGCTGCTGAGCAGATTC 556
567 CAAAATFACCACTTGGGCTTACAGAGGAGAGCAGTCCGATGCTGCTGAGCAGATTC 626
567 CAAAATFACCACTTGGGCTTACAGAGGAGAGCAGTCCGATGCTGCTGAGCAGATTC 626

QY 557 TGTGTGCGGGGAACACCCGGAGGACTCATGCCAGGGCGACTCCGGAGGGCCCTGTGGT 616
 DB 627 TGTGTGCGGGGAACACCCGGAGGACTCATGCCAGGGCGACTCCGGAGGGCCCTGTGGT 686
 QY 617 GCAAGGTGAATGGACCTGTGGCTGCGAGGGGGGTGTGCTGAGCTGGGGCCAGAGGCTGTGGCC 676
 DB 687 GCAAGGTGAATGGACCTGTGGCTGCGAGGGGGGTGTGCTGAGCTGGGGCCAGAGGCTGTGGCC 746
 QY 677 AGCCCAACCGGCTGTCATCTACCCCGTGTACCTGACTTGGACTGGATCCACCACT 736
 DB 747 AGCCCAACCGGCTGTCATCTACCCCGTGTACCTGACTTGGACTGGATCCACCACT 806
 QY 737 ATGTCCCAAAAAAGCCGTGAGAGCGCC 763
 DB 807 ATGTCCCAAAAAAGCCGTGAGAGCGCC 833

RESULT 3

US-08-978-404B-15
 ; Sequence 15, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FLBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: IBM Compatible
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELETYPE:
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1128 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-978-404B-15

Query Match 94.8%; Score 731; DB 2; Length 1128;
 Best Local Similarity 98.7%; Pred. No. 6e-157;
 Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 17 GAATCGTGGGGGTGAGAGGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCCTGAGAG 76
 DB 87 GCATCTTGGGGGTGAGAGGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCCTGAGAG 146
 QY 77 TCCAGGCCCCATACGAGTGCATCTTGTGGGGGGCTCCCTCATCCACCCCAAGTGGGTG 136
 DB 147 TCCAGGCCCCATACGAGTGCATCTTGTGGGGGGCTCCCTCATCCACCCCAAGTGGGTG 206

QY 137 TCACCCCGCGGCGGTGTGCTGGAGCCGGAGCTGAAGATGTGGCCCGCTCAGGCTGCAAC 196
 DB 207 TCACCCCGCGGCGGTGTGCTGGAGCCGGAGCTGAAGATGTGGCCCGCTCAGGCTGCAAC 266
 QY 197 TCGGGGAGGACCACTCTACTACAGAGACCACTGTGCTGGCGGTCAAGAGATCATGTGTC 256
 DB 267 TCGGGGAGGACCACTCTACTACAGAGACCACTGTGCTGGCGGTCAAGAGATCATGTGTC 326
 QY 257 ACCCAAGTGTACACCCCGGAGTGGAGGAGAACATGGCCGTGGGAGTGGAGGAGC 316
 DB 327 ACCCAAGTGTACACCCCGGAGTGGAGGAGAACATGGCCGTGGGAGTGGAGGAGC 386
 QY 317 CGGTGAAGTGTCCAGCCACAGTCCACAGCCAGTCCAGCCCTGCTGCTGAGAGAGAGC 376
 DB 387 CGGTGAAGTGTCCAGCCACAGTCCACAGCCAGTCCAGCCCTGCTGCTGAGAGAGAGC 446
 QY 377 CCCCCGGGATGCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
 DB 447 CCCCCGGGATGCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
 QY 437 CACCCGATTTCTTCCGTAAGGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 496
 DB 507 CACCCGATTTCTTCCGTAAGGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 566
 QY 497 CAAAATACCACCTTGGCGCTACACGGGAGAGAGTCCCGCATTCCTGTGACAGCATGC 556
 DB 567 CAAAATACCACCTTGGCGCTACACGGGAGAGAGTCCCGCATTCCTGTGACAGCATGC 626
 QY 557 TGTGTGCGGGGAACACCCGGAGGACTCATGCCAGGGCGACTCCGGAGGGCCCTGTGGT 616
 DB 627 TGTGTGCGGGGAACACCCGGAGGACTCATGCCAGGGCGACTCCGGAGGGCCCTGTGGT 686
 QY 617 GCAAGGTGAATGGACCTGTGGCTGCGAGGGGGGTGTGCTGAGCTGGGGCCAGAGGCTGTGGCC 676
 DB 687 GCAAGGTGAATGGACCTGTGGCTGCGAGGGGGGTGTGCTGAGCTGGGGCCAGAGGCTGTGGCC 746

RESULT 4

US-09-016-366A-18
 ; Sequence 18, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: IBM Compatible
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090

QY 737 ATGTCCCAAAAAAGCCGTGAGAGCGCC 763
 DB 807 ATGTCCCAAAAAAGCCGTGAGAGCGCC 833

FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO.: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-016-366A-18

Query Match 94.8%; Score 731; DB 2; Length 1137;
Best Local Similarity 98.7%; Pred. No. 6e-157;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

17 GAATGCTGGGGGTGAGAGAGGCCCCAGGAGCAAGTGGCCCTGGGAGGTGACCTGAGAG 76
85 GCATGCTGGGGGTGAGAGAGGCCCCAGGAGCAAGTGGCCCTGGGAGGTGACCTGAGAG 144
77 TCCAGGGCCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
145 TCCAGGGCCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
137 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 196
205 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 264
197 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 256
265 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 324
257 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 316
325 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 384
317 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 376
385 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 444
377 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 436
445 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 504
437 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 496
505 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 564
497 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 556
565 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 624
557 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 616
625 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 684
617 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 676
685 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 744
677 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 736
745 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 804
737 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 763
805 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 831

RESULT 5
US-08-978-404B-13
Sequence 13, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FTBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P. C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: B0801/7090
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-13

Query Match 94.8%; Score 731; DB 2; Length 1137;
Best Local Similarity 98.7%; Pred. No. 6e-157;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

17 GAATGCTGGGGGTGAGAGAGGCCCCAGGAGCAAGTGGCCCTGGGAGGTGACCTGAGAG 76
85 GCATGCTGGGGGTGAGAGAGGCCCCAGGAGCAAGTGGCCCTGGGAGGTGACCTGAGAG 144
77 TCCAGGGCCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
145 TCCAGGGCCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
137 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 196
205 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 264
197 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 256
265 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 324
257 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 316
325 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 384
317 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 376
385 TGAACCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 444

QY 77 TCACGGCCCATACTGATGATGCACTTTCGCGGGGGCTCCCTCATCCACCACCAGTGGGTGC 136
 Db 126 TCCGGACCCGAACTGGATGGATGCACTTCTGCGGGGGGGCTCCCTCATCCACCACCAGTGGGTGC 185
 QY 137 TGACCGCCCGGGGGCTGGCTGGAGCCCGGACGTCAMAGATCTGGCCCTCAAGGTGCAAC 196
 Db 186 TGACCGCCCGGGGGCTGGAGCCCGGACGTCAMAGATCTGGCCCTCAAGGTGCAAC 245
 QY 197 TGGCGGACACACACCTCTACTACAGAGACAGCTGCTGCGGGGTCGACAGGATCATGCTG 256
 Db 246 TGGCGGACACACACCTCTACTACAGAGACAGCTGCTGCGGGGTCGACAGGATCATGCTG 305
 QY 257 ACCCAGACTTCTACACCCCGCAGATCGAGCCGAGACATCCCTCTGAGGCTGAGAGAGC 316
 Db 306 ACCCAGACTTCTACACCCCGCAGATCGAGCCGAGACATCCCTCTGAGGCTGAGAGAGC 365
 QY 317 GGGTGAAGTCTCCAGCCAGCTCCACAGGTCACCTCCCTCCCTCCAGACCTTCC 376
 Db 366 GGGTGAAGTCTCCAGCCAGCTCCACAGGTCACCTCCCTCCCTCCAGACCTTCC 425
 QY 377 CCGCGGGGATGCGCTGCTGGGTCACTGGCTGGGGGATGATGAGACAAATGATGAGCGCTCC 436
 Db 426 CCGCGGGGATGCGCTGCTGGGTCACTGGCTGGGGGATGATGAGACAAATGATGAGCGCTCC 485
 QY 437 CACCGCCATTTCTCTGAGAGCAGTGAAGTCCCATTAATGAGAAAACCAATTTGTGAGC 496
 Db 486 CACCGCCATTTCTCTGAGAGCAGTGAAGTCCCATTAATGAGAAAACCAATTTGTGAGC 545
 QY 497 CAAAATACCACTTGGGGCTTACAGAGGAGACAGCTCCGATGCTGCTGAGCAGATGC 556
 Db 546 CAAAATACCACTTGGGGCTTACAGAGGAGACAGCTCCGATGCTGCTGAGCAGATGC 605
 QY 557 TGTGTGCGGGGAAACCCCGGAGGAGCATGATGACAGGGGACATCCGGAGGGCCCGTGGT 616
 Db 606 TGTGTGCGGGGAAACCCCGGAGGAGCATGATGACAGGGGACATCCGGAGGGCCCGTGGT 665
 QY 617 GCAAGGTGAATGGACACTGGCTGCAAGCGGGGCTGGTCAAGTGGGGGCGAGGGCTGTGCC 676
 Db 666 GCAAGGTGAATGGACACTGGCTGCAAGCGGGGCTGGTCAAGTGGGGGCGAGGGCTGTGCC 725
 QY 677 AGCCCAACCGGCTGGCATCTACACCCCTGTACACTACTTGGACTGGATCCACT 736
 Db 726 AGCCCAACCGGCTGGCATCTACACCCCTGTACACTACTTGGACTGGATCCACT 785
 QY 737 ATGTCCCAAAAAAGCCGTGAAGGGCC 763
 Db 786 ATGTCCCAAAAAAGCCGTGAAGGGCC 812

FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037, 090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELETYPE:
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-016-366A-16

Query Match 89.0%; Score 686.2; DB 2; Length 1154;
 Best Local Similarity 94.3%; Pred. No. 8.2e-147;
 Matches 712; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 17 GAATGTCGGGGGTCAGGAGGCCCCCAGGACAGTGGCCCTGGAGGAGGAGCTGAGAG 76
 Db 106 GATGTCGGGGGTCAGGAGGCCCCCAGGACAGTGGCCCTGGAGGAGGAGCTGAGAG 165
 QY 77 TCACGGCCCATACTGATGATGCACTTTCGCGGGGGCTCCCTCATCCACCACCAGTGGGTGC 136
 Db 166 TCCGGACCCGAACTGGATGGATGCACTTCTGCGGGGGGGCTCCCTCATCCACCACCAGTGGGTGC 225
 QY 137 TGACCGCCCGGGGGCTGGCTGGAGCCCGGACGTCAMAGATCTGGCCCTCAAGGTGCAAC 196
 Db 226 TGACCGCCCGGGGGCTGGAGCCCGGACGTCAMAGATCTGGCCCTCAAGGTGCAAC 285
 QY 197 TGGCGGACACACACCTCTACTACAGAGACAGCTGCTGCGGGGTCGACAGGATCATGCTG 256
 Db 286 TGGCGGACACACACCTCTACTACAGAGACAGCTGCTGCGGGGTCGACAGGATCATGCTG 345
 QY 257 ACCCAGACTTCTACACCCCGCAGATCGAGCCGAGACATCCCTCTGAGGCTGAGAGAGC 316
 Db 346 ACCCAGACTTCTACACCCCGCAGATCGAGCCGAGACATCCCTCTGAGGCTGAGAGAGC 405
 QY 317 GGGTGAAGTCTCCAGCCAGCTCCACAGGTCACCTCCCTCCCTCCAGACCTTCC 376
 Db 406 GGGTGAAGTCTCCAGCCAGCTCCACAGGTCACCTCCCTCCCTCCAGACCTTCC 465
 QY 377 CCGCGGGGATGCGCTGCTGGGTCACTGGCTGGGGGATGATGAGACAAATGATGAGCGCTCC 436
 Db 466 CCGCGGGGATGCGCTGCTGGGTCACTGGCTGGGGGATGATGAGACAAATGATGAGCGCTCC 525
 QY 437 CACCGCCATTTCTCTGAGAGCAGTGAAGTCCCATTAATGAGAAAACCAATTTGTGAGC 496
 Db 526 CACCGCCATTTCTCTGAGAGCAGTGAAGTCCCATTAATGAGAAAACCAATTTGTGAGC 585
 QY 497 CAAAATACCACTTGGGGCTTACAGAGGAGACAGCTCCGATGCTGCTGAGCAGATGC 556
 Db 586 CAAAATACCACTTGGGGCTTACAGAGGAGACAGCTCCGATGCTGCTGAGCAGATGC 645
 QY 557 TGTGTGCGGGGAAACCCCGGAGGAGCATGATGACAGGGGACATCCGGAGGGCCCGTGGT 616
 Db 646 TGTGTGCGGGGAAACCCCGGAGGAGCATGATGACAGGGGACATCCGGAGGGCCCGTGGT 705
 QY 617 GCAAGGTGAATGGACACTGGCTGCAAGCGGGGCTGGTCAAGTGGGGGCGAGGGCTGTGCC 676
 Db 706 GCAAGGTGAATGGACACTGGCTGCAAGCGGGGCTGGTCAAGTGGGGGCGAGGGCTGTGCC 765
 QY 677 AGCCCAACCGGCTGGCATCTACACCCCTGTACACTACTTGGACTGGATCCACT 736
 Db 766 AGCCCAACCGGCTGGCATCTACACCCCTGTACACTACTTGGACTGGATCCACT 825

RESULT 9
 US-09-016-366A-16
 : Sequence 16, Application US/09016366A
 : Patent No. 5955431
 : GENERAL INFORMATION:
 : APPLICANT: Stevens, Richard L.
 : APPLICANT: Huang, Chifu
 : TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 : TITLE OF INVENTION: INHIBITORS
 : NUMBER OF SEQUENCES: 65
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 : STREET: 600 Atlantic Avenue
 : CITY: Boston
 : STATE: MA
 : COUNTRY: U. S. A.
 : ZIP: 02210-2211
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/016,366A

QY 737 ATGTCCCAAAAAGCCGTGAMCGCGCCGCGCTGCF 771
 Db 826 ATGTCCCAAAAAGCCGTGAGTCAGCGCCGCGGTGT 860

RESULT 10
 US-08-978-404B-11
 : Sequence 11, Application US/08978404B

GENERAL INFORMATION:
 : APPLICANT: Stevens, Richard L.
 : TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 : TITLE OF INVENTION: FIBRINOGEN
 : NUMBER OF SEQUENCES: 74
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Wolf, Greenfield & Sacks, P.C.
 : STREET: 600 Atlantic Avenue
 : CITY: Boston
 : STATE: MA
 : COUNTRY: U.S.A.
 : ZIP: 02210-2211

COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/978,404B
 : FILING DATE: 25-NOV-97
 : CLASSIFICATION: 435
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: 60/032,354
 : FILING DATE: 04-DEC-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Plumer, Elizabeth R.
 : REGISTRATION NUMBER: 36,637
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-720-3500
 : TELEFAX: 617-720-2441

TELEX:
 : INFORMATION FOR SEQ ID NO: 11:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1154 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-978-404B-11

Query Match 89.0%; Score 686.2; DB 2; Length 1154;
 Best Local Similarity 94.3%; Pred. No. 8.2e-147;
 Matches 712; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 17 GAATGTCGGGGGTCAGAGAGCCCAAGAGCAAGTGGCCCTGCGAGGTGAGCCTGAAG 76
 Db 106 GATGTCGGGGGTCAGAGAGCCCAAGAGCAAGTGGCCCTGCGAGGTGAGCCTGAAG 165
 QY 77 TCCAGCGGCCAATACGAMGACACTTCTGGGGGCTCCCTCATCCACCCCAAGTGGGTGC 136
 Db 166 TCCAGCGGCCAATACGAMGACACTTCTGGGGGCTCCCTCATCCACCCCAAGTGGGTGC 225
 QY 137 TGACCGCGCGCGCGTGGGACCGGACGTCAGAGATCTGGCCCGCTCAGGGTGC 196
 Db 226 TGACCGCGCGCGCGTGGGACCGGACGTCAGAGATCTGGCCCGCTCAGGGTGC 285
 QY 197 TCGCGGACAGCACCTCTACTACAGAGACCAAGCTGCGCGGTGACAGAGATCATCTGTC 256
 Db 286 TCGCGGACAGCACCTCTACTACAGAGACCAAGCTGCGCGGTGACAGAGATCATCTGTC 345
 QY 257 ACCCACAGTTCTACACCGCCCAAGTCCGAGAGGAGATGCGCCCTGCTGAGCTGAGGAGAC 316
 Db 346 ACCCACAGTTCTACACCGCCCAAGTCCGAGAGGAGATGCGCCCTGCTGAGGAGGAGAC 405

QY 317 CGGTGAAGGTCTCCAGCCAGTCACACAGGTCACCCCTGCCCCCTGCTCAGAGACTTTC 376
 Db 406 CCGTGAACATCTCCAGCGCGCCGTCACACAGGTCATCTGCTCCCGCTGCGGAGACTTTC 465
 QY 377 CCGCGGGATGCGCGTGTGGTCTACTGCTGGGGCGATGTGGACATATGAGCGCCCTCC 436
 Db 466 CCGCGGGATGCGCGTGTGGTCTACTGCTGGGGCGATGTGGACATATGAGCGCCCTCC 525
 QY 437 CACCGCCATTTCCCTGAAAGGAGGTCGCCCATATATGAAACCAACATTTCTGACG 496
 Db 526 CACCGCCATTTCCCTGAAAGGAGGTCGCCCATATATGAAACCAACATTTCTGACG 585
 QY 497 CAAATFACACCTTTGGCCCTTACACAGGAGACGAGCTCCGATCCGTGACAGCATGC 556
 Db 586 CAAATFACACCTTTGGCCCTTACACAGGAGACGAGCTCCGATCCGTGACAGCATGC 645
 QY 557 TGTGTCCGGGAAACACCCGGAGGACTATGACAGGCGGACTCGGAGGGCCCTGCTGT 616
 Db 646 TGTGTCCGGGAAACACCCGGAGGACTATGACAGGCGGACTCGGAGGGCCCTGCTGT 705
 QY 617 GCAAGTGAATGACACCGTGGCTGACAGGGGGGGGTGATGCTGGGGCGAGGGCTTGGCC 676
 Db 706 GCAAGTGAATGACACCGTGGCTGACAGGGGGGGGTGATGCTGGGGCGAGGGCTTGGCC 765
 QY 677 AGCCCAACCGCGCTGCACTTACACCCGCTGTCACCTACTTGTGACTGATCCACACT 736
 Db 766 AGCCCAACCGCGCTGCACTTACACCCGCTGTCACCTACTTGTGACTGATCCACACT 825
 QY 737 ATGTCCCAAAAAGCCGTGAMCGCGCCGCGCTGCF 771
 Db 826 ATGTCCCAAAAAGCCGTGAGTCAGCGCCGCGGTGT 860

RESULT 11
 US-08-978-404B-7
 : Sequence 7, Application US/08978404B
 : Patent No. 5968782
 : GENERAL INFORMATION:
 : APPLICANT: Stevens, Richard L.
 : TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 : TITLE OF INVENTION: FIBRINOGEN
 : NUMBER OF SEQUENCES: 74
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Wolf, Greenfield & Sacks, P.C.
 : STREET: 600 Atlantic Avenue
 : CITY: Boston
 : STATE: MA
 : COUNTRY: U.S.A.
 : ZIP: 02210-2211
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/978,404B
 : FILING DATE: 25-NOV-97
 : CLASSIFICATION: 435
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: 60/032,354
 : FILING DATE: 04-DEC-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Plumer, Elizabeth R.
 : REGISTRATION NUMBER: 36,637
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-720-3500
 : TELEFAX: 617-720-2441

TELEX:
 : INFORMATION FOR SEQ ID NO: 7:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1219 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-7

Query Match 61.9%; Score 477.2; DB 2; Length 1219;
Best Local Similarity 77.1%; Pred. No. 1.6e-99;
Matches 581; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

6 CCTGAGAAAAGATGTCGCGGGGTCAGGAGGCCCCCAAGAGCAGAGTGGCCCTGGCAGGT 65
260 CCAAGAGGGGGCATTTGGGGGACAGAGGACACCTGGGAAACAAGTGGCCCTGGCAGGT 319
66 GAGCCTGAGAGTCCAGGGCCCATCTGATGATGATGATGATGATGATGATGATGATGAT 125
320 GAGCCTTGGTGCATGAAACCTACTGAGGAGCATTTTCGCGGGCTCCCTCATTCACCC 379
126 CCAATGGGTGCTGACCCGGCGGGCGTGGTGGGAGCCGCAAGATGTCGCGCCCT 185
380 ACAGTGGGTGCTCACCGGGGACACTGTGTGGGACCCGACTATTGCTGATCCCAAGGT 439
186 CAGGTGGAACGTCGGGAGCCAGCCACTTACTACAGGAGCCAGTGCCTGCCGTAGCAG 245
440 CAGAGTACAGCTTCAAAAGCAGTACTACTACTACTACTACTACTACTACTACTACTACT 499
246 GATCATCGTCCAGCCACAGATTCCTACACCGCCAGATCGGAGATCGCCCTGCTGGA 305
500 GATCATCACACACCCAGATTCCTACTACTACTACTACTACTACTACTACTACTACTACT 559
306 GCTGGAGAGCCGGTGAAGGTCCTCCAGCCACGTCACACAGGTCACCCCTGCCCTC 365
560 GCTCAAGAACCCTGTAACAATTTCCAGCCATGTCACCCCTGCCCTGCCCTGCCCTC 619
366 AGAGACCTTCCCGGGGATCCCTGCTGGTCACTGCTGGGGGCGATGTGAAATGA 425
620 AGAGACCTTCCCGGGGATCCCTGCTGGTCACTGCTGGGGGCGATGTGAAATGA 679
426 TGAGCCCTCCAGCCATTTCTCTGTGAAGCAGGTGAAGTCCCATTAATGAAACCA 485
680 TGTAGGCTCCAGCCATTTCTCTGTGAAGCAGGTGAAGTCCCATTAATGAAACCA 739
486 CATTTGTGACGCAAAATACACACTTGGGGCTTACACAGGAGACGACGTCCGATGCTCC 545
740 GCTTTGTGACGCAAAATACACACTTGGGGCTTACACAGGAGACGACGTCCGATGCTCC 799
546 TGAGACACATGCTGTCGGCGGGAACACCCGGAGGACATCCATCCAGGGGACTCCGGAG 605
800 AGACGACATGCTGTCGGCGGGAACACCCGGAGGACATCCATCCAGGGGACTCCGGAG 859
606 GCGCCCTGATGCAAGATGATGACACCTGGCTGCAGGGGCGGTGTCAGCTGGGGCGA 665
860 ACCCTGCTGTCAGAGATGATGACACCTGGCTGCAGGGGCGGTGTCAGCTGGGGCGA 919
666 GGGCTGTGCCAGCCAAACCGGCTGGCATCTACACCCGTTGACCTACTACTGAGACTG 725
920 GGGCTGTGCCAGCCAAACCGGCTGGCATCTACACCCGTTGACCTACTACTGAGACTG 979
726 GATTCACACATGTCGTCGCAAAACCGGCTGAAAGC 759
980 GATTCACACATGTCGTCGCAAAACCGGCTGAAAGC 1013

RESULT 12
US-09-016-366A-14
Sequence 14, Application US/09016366A
Patent No. 5953431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ. ID NO.: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-016-366A-14

Query Match 50.9%; Score 469.6; DB 2; Length 1108;
Best Local Similarity 77.2%; Pred. No. 8.1e-98;
Matches 571; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

17 GAATCGTGGGGGTAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGTGGAGCTGAGAG 76
125 GATCGTGGGGGTAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGTGGAGCTGAGAGT 184
77 FCACGGCCCATCATGATGATGACCTTCTGGGGGGGCTCCCTCATCCACCCCGGATGCT 136
185 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 244
137 TGACCCCGGCGGCTGCGTGGGAGCCGACATCAAGATCTGGCCCGCTCAAGGTCGCAAC 196
245 FCACGGCCCATCATGATGATGACCTTCTGGGGGGGCTCCCTCATCCACCCCGGATGCT 304
197 TCGGGGAGCAGCAGCTCTACTACTACTACTACTACTACTACTACTACTACTACTACT 256
305 TTCGAGGAGCAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 364
257 ACCCAGATTTCAACCCGGCCAGATCGGAGGAGGAGCAGATCGCCCTGGCGGAGGAGGAGC 316
365 ACCCCAGATTTCAACCCGGCCAGATCGGAGGAGGAGCAGATCGCCCTGGCGGAGGAGGAGC 424
317 CCGTGAAGGTCTCCAGCCAGCTCCACACAGGTCACCCCTGGCCCTCCCTCAGAGACTTCC 376
425 CTTGTAAGTCTCCAGCCAGCTCCACACAGGTCACCCCTGGCCCTCCCTCAGAGACTTCC 484
377 CCGCGGGGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
485 CCGCTGGGAGCAGTGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 544
437 CACCGCATTTCTGTCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 496
545 CACTCTCTTATCTCTGAGAGCAAGTGAAGTTCCCATTTGTAAGAAACAGCCTGTGTGACC 604
497 CAATTAACACCTTGGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 556


```

APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-978-404B-1

```

```

Query Match          60.1%; Score 463; DB 2; Length 1031;
Best Local Similarity 76.4%; Pred. No. 2,5e-96;
Matches 568; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

```

```

14 AAGAATCGTCGGGGTACAGGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTAGACCTGA 73
106 AAGGATTGTGGGGGACAGGAGGCAACATGGGAACAAGTGCCCTGGCAGGTAGACCTGC 165
74 GAGTCCAGGCGCCATACAGTATCTTGTGGGGGCTCCCTCATCCACCCCTCAGGGTGG 133
166 GAGCCAAATGACACCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 225
134 TCGTACCCCGCCCGCCGCTGCTGGAGCCGAGCTCAAGGATGTGGCCCTCAGGGTGC 193
226 TCGTACTGCGGGACACAGTGTGGAGCCGGATGTGTGTGTGTGTGTGTGTGTGTGTGT 285
194 AACTGGGGAGAGCAACCTCTACACAGAGCAAGGAGCAGCTGCTGCGGTGACAGATCAG 253
286 AACTGCGGAGAGTACCTCTATACAGAGCAAGGAGCAGCTGCTGCGGTGACAGATCAG 345
254 TGCACCCACAGTTCACACCCGCGAGATGGAGGCGGACATGCGCCCTGCGGAGCTGGAG 313
346 CACACCCCGCATTCTACATCGTCCAGAGATGGGGCAGACATGCGCCCTGGAACACTCACA 405
314 ACCCGGTAAGGCTTCCAGCCACGTCACACCGTCAACCTGCCCCCTGCGCTCAGAGACT 373
406 ACCCGTGAACATTTCTGACTATGTCCACCCCTGCTCCCTTACTCTGCTGCTGAGAGACT 465
374 TCCCGCCGGGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
466 TCCCGTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 525
434 TCCCGCCCGCATTCTCTGGAAGCAGGTGAAGTCCCTCATTAATGGAACCAATTTTGTG 493
526 TCCCGCCCGCATTCTCTTGAAGAGGTGCAAGTTCCCTTTATGAAACCACTTTTGTG 585
494 AGCAAAAATACCACCTTGGCGCCCTACAGCGAGAGCAAGCAAGCTGCGCATGCGGTGAGACA 553
586 ACTTGAATGATACAAGAGTCTATACAGAGTGCACAAATGTCACATTTGTCCAGATGACA 645
554 TCGTGTGTCCGGGAAACACCCGAGGAGACTCATGCCAGGCGACTCCGGAGGGCCCCCTGG 613
646 TCGTGTGTCTGGGAATGAAAGCAATGACTCTCCAGGGGACTCCGGAGGAAACCTGTCG 705
614 TGTGAAGTGAATGGCAACCTGGCTGCAAGCGGGGGGTGTGAGCTGGGGCGAGGGCTGTG 673
706 TGTGGAAGGATGAAGACACTGGCTGGCAGGCGTGTGACGTGGGGGTGAGGGCTGTG 765
674 CCCAAGCCAAACCGGCTGATCTACACCCGATGCACTACTACTGATGATGATGATGATG 733
766 CACAGGCCAAAGCGCTGGGATCTTACACCCGGGTGACACTTATTTGACTGGATTCACC 825
734 ACTATGTCCCAAAAACCGGTGA 756
826 ACTATGTCCCAAAAACCGGTGA 848

```

```

RESULF 15
US-09-016-366A-24
Sequence 24, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-24

```

```

Query Match          57.8%; Score 445.6; DB 2; Length 1103;
Best Local Similarity 75.1%; Pred. No. 2.2e-92;
Matches 556; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
17 GAATGCTGGGGGTGAGAGGCCCCAGAGCAAGTGGCCCTGCGAGGAGCTGAGAG 76
102 GCAATGTTGGGAGAGGAGGAGGGCTTCTGAAGTAAAGTGGCCCTGGCAGGATGAGAT 161
77 TCCAGGCCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
162 TTAATTCAGTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 221
137 TGACCGCGCGGGCGTGGGAGCCGAGCGCAAGATCTGCGCCCGCTCAGGGTGAAC 196
222 TCACTGGCGGACACTGTGTGGGAGCTGCACATGAAAAAGCCCAAGCTTTCGTTGAC 281
197 TCGGGAGGACAGCACTTACTACAGAGCACAGCTGCTGGCTGAGCAAGATCATGTC 256
282 TTCGAGAGAGTATATATATATATATATATATATATATATATATATATATATATAT 341
257 ACCCACATGTTCTACACCCCGCAGATGGAAGCGGAGATGCGCCCTGCTGAGCTGAGAG 316
342 ACCCCCACTACTACACAGTGTGAGATGGGGAGATGGCGAGACATGTCCTGCTGGTGGAGAAC 401
317 CGGTGAAGTCTCCAGCCAGTCCAGCGGTCACACCCCTGCCCCCTGCTGCTGAGAGACTTCC 376

```

```

Db 402 CTGTGAATGTCTCCACCCATATCCACCCACATVCCCTGCCCTCCGAGACTTCC 461
OY 377 CCCCCGGGATGCGCGTGGGGTCACTGGGCTGGGGGATGGGACATGATGAGCGCCCTCC 436
Db 452 CCTCGGGGACTTCTTGTGGTAAAGGACAGCGCTGGGCGGACATTTGATGAGAGCCCTCC 521
OY 437 CACCGCCATTTCCTCTGAAAGCAGGTGAAGGTCCCAATAATGGAAAACCAATTTGTGACG 496
Db 522 TGCCACCTTATCTCTGAAGCAAGTGAAGGTCCCATTTGGTGAACAGCCCTGTGATC 581
OY 497 CAAAATACGACCTTTGGCGCTTACAGGGGAGAGAGCTCCGATCCGTCCGTGACGATGC 556
Db 582 GGAAGTACCCACACTGCGCTTACACAGGAGATGTTCCTCCAGATGGCATGC 641
OY 557 TGTGTCCGGGAAACACCCGGAGGAGACTATGCCAGGGCCACTCCGAGGGCCCTGGTGT 616
Db 642 TGTGTCTGGAATAATCCAGAGCGACTCCTGCCAAGGAGACTCAAGGGGCCCTGTGTCT 701
OY 617 GCAAGGTGAATGGCACCTGGCTGCAAGCGGGCCGTGCTCACTGGGGCCGAGGGCTGTGCC 676
Db 702 GCAAGGTGAAGGGTACTGCTGAGGTCGAAGCAGAGAGTGTGACTGGGGCCGAGGGCTGCGAG 761
OY 677 AGCCCAACCGGCTTGGCACTTACACCCGTGTGACTACTTGGACTGATCCACACT 736
Db 762 AGGCCAATCGTCTGGCATTTACACCCGGGTGACGTACTACTGGACTGATTCACCCGCT 821
OY 737 ATGTCCCAAAAAAGCCGTGA 756
Db 822 ATGTCCCTCAGCGTTCTGA 841

```

Search completed: January 31, 2003, 05:25:27
 Job time : 72 secs

GenCore version 5.1.3
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 05:19:45 ; Search time 2210 Seconds
 (without alignments)
 5650.100 Million cell updates/sec

Title: US-09-598-982-20
 Perfect score: 771
 Sequence: 1 gggccctcgcgagaagaat.....cgtcgaagcggcgcgcgcgtcgt 771

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
 Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

- Database :
- 1: em_estba:**
 - 2: em_esthum:**
 - 3: em_estlm:**
 - 4: em_estmu:**
 - 5: em_estov:**
 - 6: em_estpl:**
 - 7: em_estro:**
 - 8: em_hnc:**
 - 9: gb_estl:**
 - 10: gb_est2:**
 - 11: gb_hnc:**
 - 12: gb_est3:**
 - 13: gb_est4:**
 - 14: gb_est5:**
 - 15: em_estfun:**
 - 16: em_estom:**
 - 17: gb_gss:**
 - 18: em_gss_hum:**
 - 19: em_gss_inv:**
 - 20: em_gss_pln:**
 - 21: em_gss_vrt:**
 - 22: em_gss_fun:**
 - 23: em_gss_mam:**
 - 24: em_gss_mus:**
 - 25: em_gss_other:**
 - 26: em_gss_pro:**
 - 27: em_gss_rtd:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	676.2	87.7	1030 14	BM919268 BM919268 AGENCCURT
2	580.2	75.3	904 14	BQ720404 BQ720404 AGENCCURT
3	495.6	64.3	502 14	BQ082929 BQ082929 K-EST0144
4	468.4	60.8	736 12	BG542089 BG542089 602571309
5	444.4	57.6	917 14	BQ721078 BQ721078 AGENCCURT
6	422.2	54.8	1000 13	BI413250 BI413250 602986390

7	420.4	54.5	639	9	AA131142
8	401.4	52.1	811	12	BG697540
9	400	51.9	678	12	BG483591
10	375	48.6	512	12	BF724180
11	351	45.5	693	14	BM991728
12	350.2	45.4	676	12	BF850308
13	349.6	45.3	692	14	BM989945
14	348	45.1	688	14	BQ003361
15	334.2	43.3	371	12	BF359130
16	314.6	40.8	379	12	BF849396
17	309.4	40.1	474	10	BM823937
18	305.8	39.7	525	13	BI775716
19	304.2	39.5	545	13	BI681216
20	289.4	37.5	291	12	BF876081
21	289.4	37.5	291	12	BF876081
22	281.6	36.5	537	14	BM708916
23	276.8	35.9	613	10	AM152343
24	273.6	35.5	411	12	BE862270
25	264.8	34.3	538	12	BE751979
26	261.4	33.9	620	9	AA049080
27	259	33.6	395	14	T84325
28	258.6	33.5	413	12	BF849397
29	253.6	32.9	377	14	BQ329260
30	252.2	32.7	282	13	BG957512
31	251.2	32.6	380	13	BG983221
32	246	31.9	676	13	BG964077
33	240.6	31.2	350	14	H44196
34	239	31.0	569	13	BI287271
35	233.6	30.3	457	14	W40969
36	232.4	30.1	573	9	AA039008
37	229.6	29.8	572	14	BM686231
38	223.6	29.0	393	12	BF850309
39	223.2	28.9	616	9	AA131322
40	220.8	28.6	540	10	AM001462
41	219	28.4	564	13	BI790523
42	217	28.1	416	12	BF192575
43	217	28.1	453	12	BF192574
44	217	28.1	464	12	BF192577
45	217	28.1	564	9	AI675311

ALIGNMENTS

RESULT 1
 BM919268
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 1030)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@pds-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMN at:
 http://image.llnl.gov
 Plate: LHAM12776 Row: f Column: 20
 High quality sequence stop: 719.
 Location/Qualifiers
 1..1030

FEATURES
 source

Db 311 ACCCAAGTTTCAACCCGCCAGATCGGAGCGGACATGCCCCCTGCTGAGCTGGAGAGCC 370
 Qy 317 CGGTGAAGGTCTCCAGCCACGTCACACAGGTCACCCCTGCCCCCTCCTCAGACCTTCC 376
 Db 371 CGGTGAAGGTCTCCAGCCACGTCACACAGGTCACCCCTGCCCCCTCCTCAGACCTTCC 430
 Qy 377 CCCCCGGGAGCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 436
 Db 431 CCCCCGGGAGCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 490
 Qy 437 CACCGCCATTTTCTCTGTAAGGAGGTAAGGTCCTCATATGTAAGCAATTTTGTGACG 496
 Db 491 CACCGCCATTTTCTCTGTAAGGAGGTAAGGTCCTCATATGTAAGCAATTTTGTGACG 550
 Qy 497 CAAATATACCCCTTGGCCCTTACACGGAGAGACGAGCTCCCGATCCGCTGACGACATGC 556
 Db 551 CAAATATACCCCTTGGCCCTTACACGGAGAGACGAGCTCCCGATCCGCTGACGACATGC 610
 Qy 557 TGTGTGGCCGGGAACACCCGGAGGACTCATGACGAGGGCCCTGCTGTGTGT 616
 Db 611 TGTGTGGCCGGGAACACCCGGAGGACTCATGACGAGGGCCCTGCTGTGTGTGTGT 670
 Qy 617 GCAAGGTGAATGACACCTGGCTGCAAGGGGGGGGT-GTTCAGCTGGGGCGAGGGCTGTGC 675
 Db 671 GCAAGGTGAATGACACCTGGCTGCAAGGGGGGGGT-GTTCAGCTGGGGCGAGGGCTGTGC 730
 Qy 676 CAGCCCAACCCGGCCCTGGATCTACACCCCGCTGACCTACTCTGG--ACTGATGCCACC 733
 Db 731 CAGCCCAACCCGGCCGG 790
 Qy 734 ACTATGTCCCCAAAAGGCC 752
 Db 791 CCTGTGGCCCCCAAGAAC 809

RESULT 3
 BQ082929 502 bp mRNA linear EST 04-APR-2002
 LOCUS K-ESF0144841 S14K402 Homo sapiens cDNA clone S14K402-59-B11 5'
 DEFINITION mRNA sequence.
 ACCESSION BQ082929
 VERSION BQ082929.1 GI:19941018
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 502)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21c Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.krribd.re.kr
 Plate: 59 row: B column: 11
 High quality sequence stop: 502.
 Location/Qualifiers
 1. 502

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S14K402-59-B11"
 /clone_lib="S14K402"
 /cell_line="K402"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pT181p1; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

BASE COUNT 99 a 170 c 148 g 85 t
 ORIGIN

Query Match 64.3%; Score 495.6; DB 14; Length 502;
 Best Local Similarity 99.2%; Pred. No. 8.3e-95;
 Matches 498; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 87 ATACTGGAGTGCATCTTGGGGGGGCTCCCTCATGCCACCCCGAGTGGTGGACGCGCG 146
 Db 1 ATACTGGAGTGCATCTTGGGGGGGCTCCCTCATGCCACCCCGAGTGGTGGACGCGCG 60
 Qy 147 GGCGTGGCGTGGGAGCGGAGCGTCAAGGATCTGGCCCGCCCTCAGGGTGCACACTGGGGAGCA 206
 Db 61 GCACGTGGCGTGGGAGCGGAGCGTCAAGGATCTGGCCCGCCCTCAGGGTGCACACTGGGGAGCA 120
 Qy 207 GCACCTTACTACACAGAGACCAAGCTGCTGCGGTACAGACAGATCATCTGACACCACAGATT 266
 Db 121 GCACCTTACTACACAGAGACCAAGCTGCTGCGGTACAGACAGATCATCTGACACCACAGATT 180
 Qy 267 CTACACCGCCCGAGATCGGAGGCGGACATGCCCTGGTGGAGCTGGAGGAGCCGTTAAGGT 326
 Db 181 CTACACCGCCCGAGATCGGAGGCGGACATGCCCTGGTGGAGCTGGAGGAGCCGTTAAGGT 240
 Qy 327 CTCCAGCCACGTCCACACAGCGTCAACCTGGCCCTGCTAGAGACCTTCCCGCCGGGGAT 386
 Db 241 CTCCAGCCACGTCCACACAGCGTCAACCTGGCCCTGCTAGAGACCTTCCCGCCGGGGAT 300
 Qy 387 GCCGTGCTGGGTTCACGTGCGTGGGGGAGTGGACAAATGATGAGCGCTCCACCGCCATT 446
 Db 301 GCCGTGCTGGGTTCACGTGCGTGGGGGAGTGGACAAATGATGAGCGCGCTCCACCGCCATT 360
 Qy 447 TCCCTGTAAGGCAAGTGAAGGTCCTCCCATATGGAAGAAACCAATTTGAGCGCAAAATATCA 506
 Db 361 TCCCTGTAAGGCAAGTGAAGGTCCTCCCATATGGAAGAAACCAATTTGAGCGCAAAATATCA 420
 Qy 507 CTTTGGCCCTTACACGGAGACGATCGCTGCTGAGACATGCTGTGGCCGG 566
 Db 421 CTTTGGCCCTTACACGGAGACGATCGCTGCTGAGACATGCTGTGGCCGG 480
 Qy 567 GAAACACCCCGAGGACTCATGC 588
 Db 481 GAAACACCCCGAGGACTCATGC 502

RESULT 4
 BGS542089 736 bp mRNA linear EST 03-APR-2001
 LOCUS 602571309F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695458 5'
 DEFINITION mRNA sequence.
 ACCESSION BGS542089
 VERSION BGS542089.1 GI:135343322
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 736)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov

Plate: LICM1521 row: b column: 03

High quality sequence stop: 725.

Location/Qualifiers

1. 736

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4695458"

/clone_lib="NIH_MGC_77"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: Lung; Vector: pDRR-LIB (Clontech); Site_1: ffl (gagccctcggcc); Site_2: ffl (gagccatcggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCCATTTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAAGAGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 138 a 236 c 242 g 120 t

Query Match 60.8%; Score 468.4; DB 12; Length 736;

Best Local Similarity 90.9%; Pred. No. 5.2e-89;

Matches 567; Conservative 0; Mismatches 46; Indels 11; Gaps 6;

17 GATGTTGGGGGTAGAGAGCCGCCAGAGCAAGTGGCCCTGGAGGTGAGAG 76
113 GCATGTTGGGGGTAGAGAGCCGCCAGAGCAAGTGGCCCTGGAGGTGAGAG 172
77 TCCAGGGCCCATATCGATGAGTGCATCTGGGGGGCCCTCATACACCCCGATGGG 136
173 TCCAGGGCCCATATCGATGAGTGCATCTGGGGGGCCCTCATACACCCCGATGGG 232
137 TGACCCCGCCGGCGTGGTGGAGCCGAGTCAAGATCTGGCCCGCCCTCAGGGTGC 196
233 TGACCCCGCCGGCGTGGTGGAGCCGAGTCAAGATCTGGCCCGCCCTCAGGGTGC 292
197 TGCGGAGAGCAGCCTCTACTACACAGGACCACTGGCGGGTCAACAGATCTGTC 256
293 TGCGGAGAGCAGCCTCTACTACACAGGACCACTGGCGGGTCAACAGATCTGTC 352
257 ACCACAGTCTACACCCGCCAGATCGAGGAGGACATGCCCTGGCGAGCGAGGAG 316
353 ACCACAGTCTACACCCGCCAGATCGAGGAGGACATGCCCTGGCGAGCGAGGAG 412
317 CGGTGAAGTCTCCAGCCAGTCCACACAGGTCACCCCTGGCCCTCAGAGACCTTGC 376
413 CGGTGAAGTCTCCAGCCAGTCCACACAGGTCACCCCTGGCCCTCAGAGACCTTGC 472
377 CGCC-GGGAGATCCGTCGTCGTCACCTGGCGGGCGATGTGACAAATGATGAGCC 435
473 CCCCCGGGGATCCGTCGTCGTCACCTGGCGGGCGATGTGACAAATGATGAGCC 532
436 CCAGCCGCTTTCCTCTGTAAGAGAGG-TGAAGTCCCCCAATGAGAAACCAATTTG 494
533 CCAGCCGCTTTCCTCTGTAAGAGAGG-TGAAGTCCCCCAATGAGAAACCAATTTG 592
495 CCAGCCGCTTTCCTCTGTAAGAGAGG-TGAAGTCCCCCAATGAGAAACCAATTTG 552
593 CGCAAAATACACCTTTGGGGCCTTAAACAGGAGGAGTCCGATTTGTCGGTGAAC 652
553 ATGCT- ---GTGTGCGGGGAAACACCCGGAGGACTCATGACAGGGCG- -ACTCCG 605

Db 653 GACATTGCTGTTGTTCGCCGGGAAACACCCGGAGGAGGACTCATGCCAGGCGGACTCCGGAGG 712
Qy 606 GCCCCTGGTGTGACAGGTAATGG 629
Db 713 GCCCCTGGTGTGACAGGTAATGG 736

RESULT 5
LOCUS B0721078
DEFINITION B0721078 917 bp mRNA linear EST 16-Jul-2002
IMAGE:6189508 5', mRNA sequence.

ACCESSION B0721078
VERSION B0721078.1 GI:21859975
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov

Plate: LHAM13586 row: n column: 05
High quality sequence stop: 609.

Location/Qualifiers

1. 917

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6189508"

/clone_lib="Lupski_sym pathetic_trunk"

/sex="male"

/tissue_type="sympathetic trunk"

/dev_stage="adult, 16 yr"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTGATCTGATGTCGAGCGGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT 178 a 335 c 240 g 164 t

Query Match 57.6%; Score 444.4; DB 14; Length 917;

Best Local Similarity 98.5%; Pred. No. 6.4e-84;

Matches 459; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

299 TECTGAGGCTGGAGGAGCGGTGAGAGTCTCCAGCCAGTCCACAGGTCACCCCTGCCCC 358
1 TCGTGGAGCTGGAGGAGCGCGGTGAGAGTCTCCAGCCAGTCCACAGGTCACCCCTGCCCC 60
Qy 359 CTGCTCAGAGACCTTCCCGCCGGGAGATGCGTGTGGGTCACTGCGTGGGGCATGTGG 418
61 CTGCTCAGAGACCTTCCCGCCGGGAGATGCGTGTGGGTCACTGCGTGGGGCATGTGG 120
419 ACAATGATGAGGGCCCTCCAGCCGATTTCTCTGTAAGAGGTTGAAGTCCCAATTAATG 478
121 ACAATGATGAGGGCCCTCCAGCCGATTTCTCTGTAAGAGGTTGAAGTCCCAATTAATG 180

QY 479 AAAACCACTTTGTGACGCAAAAATACCACTTTGGCCCTACACGGGAGACGACTCCGCA 538
 Db 181 AAAACCACTTTGTGACGCAAAAATACCACTTTGGCCCTACACGGGAGACGACTCCGCA 240
 QY 539 TCGTCCGTGACGCA-GATGCTGTGTCCGGGAACACCCGGAGGACTCATGCCAGGCGAC 597
 Db 241 TCGTCCGTGACGCA-GATGCTGTGTCCGGGAACACCCGGAGGACTCATGCCAGGCGAC 300
 QY 598 TCCGGAGGCCCCCTGTGTGCAAGTGAATGGACCTGGCTGGCCAGGCGGGGTGGTCCAGC 657
 Db 301 TCCGGAGGCCCCCTGTGTGCAAGTGAATGGACCTGGCTGGCCAGGCGGGGTGGTCCAGC 360
 QY 658 TGGGGCGAGGGCTGTGCCACGCAACCGGCTGGCATCTACACCCGCTGTCACTACTAC 717
 Db 361 TGGGGCGAGGGCTGTGCCACGCAACCGGCTGGCATCTACACCCGCTGTCACTACTAC 420
 QY 718 TTGGACTGATTCACCACTATGTCCCAAAAAAGCCGTGAAGCGGCC 763
 Db 421 TTGGACTGATTCACCACTATGTCCCAAAAAAGCCGTGAAGCGGCC 466

RESULT 6
 LOCUS B1413250 1000 bp mRNA linear EST 14-AUG-2001
 DEFINITION 602986390F1 NCI_GCAP_Lu33 Mus musculus cDNA clone IMAGE:5142478 5',
 mRNA sequence.
 ACCESSION B1413250
 VERSION B1413250
 KEYWORDS GI:15174173
 SOURCE EST.
 ORGANISM house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1000)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@bglbmail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-GCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM11351 Row: C Column: 23
 High quality sequence start: 32
 High quality sequence stop: 849.
 Location/Qualifiers

FEATURES
 source 1..1000
 /organism="Mus musculus"
 /strain="CEBCH 11"
 /db_xref="taxon:10090"
 /clone="IMAGE:5142478"
 /clone_lib="NCI_GCAP_Lu33"
 /issue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Lung; Vector: pVT3b-Pac (Pharmacia) with a
 modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
 strand cDNA was prepared from mRNA obtained from pooled
 lung tumors with a Not I - oligo(dT) primer [5',
 TGTTACCAATCTGAAAGTGGAGCGCGCCCTCTTTTCTTTTCTTTT
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pVT3b vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 202 a 294 c 274 g 229 t 1 others
 Query Match 54.8%; Score 422.2; DB 13; Length 1000;

Best Local Similarity 77.2%; Pred. No. 3.2e-79;
 Matches 564; Conservative 0; Mismatches 163; Indels 4; Gaps 4;

QY 17 GAATGCTGGGGGTGACGAGGCGCCCGCAGGCAAGTGGCCCTGGCAGGTGAGAG 76
 Db 73 GCATGTGGGAGACATGCTTCTGAGATGAGTGGCCCTGGCAGGTGAGAGT 132
 QY 77 TCCAGGCGCCATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
 Db 133 TTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 192
 QY 137 TGACCCCGCGGGCTGTGCGGTGCGGAGCAGTCAAGATCTGGCCCGCCTCAGGGTCAAC 196
 Db 193 TCACTGGCGGACACGCTGTGGGAGCCGACATCAAAAAGCCACAGGCTCTTCGGGGTGCAGC 252
 QY 197 TGGGGAGCAGCAGCCTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 256
 Db 253 TTCTGTGAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
 QY 257 ACCCAGATTTTACACCCCGCCAGATCGGAGGAGACATGCGCCCTGGTGGAGGCTGGGAGGAGC 316
 Db 313 ACCCCACTATTACACCGCCGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 372
 QY 317 CGGTGAAGGTTCTCCAGCCACGTCACACGTCACACCCCTGGCCCTGCTCAGAGACTTTC 376
 Db 373 CTGTGAATGTTCTCCAGCCACATATCCACACCCCTGGCCCTGCTCAGAGACTTTC 432
 QY 377 CCGGGGGGATGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
 Db 433 CCGGGGGGATGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
 QY 437 CAGCGCAATTTCTCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 495
 Db 493 CAGCTCTTATATCTCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
 QY 496 GCAAAATATCACCTTTGGGCTTACACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 555
 Db 553 GGAAGTAAACACACGCGGCTCTTACACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 612
 QY 556 CTGTGTCCGGGAGACACCCGGAGGAGCTGATGTCACAGGGCGACTCCGGAGGGCCCTGGTGTG 615
 Db 613 CTGTGTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 672
 QY 616 TGCAGAGTGAATGGAACCTGGCTGACAGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 674
 Db 673 TGCAGAGTGAATGGAACCTGGCTGACAGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
 QY 675 CCAGCCC-AACCGGCTGGCATCTACACCCGCTGTCACC-TACTACTTGGACTGGATATCCAC 732
 Db 733 ACAGCCCAAAACAGCCCTGGCATCTACACCCGCTGTCACC-TACTACTTGGACTGGATATCCAC 792

RESULT 7
 LOCUS AA131142 639 bp mRNA linear EST 14-MAY-1997
 DEFINITION 12131b01.r1 Soares_pregnant_uterus_Nb1P1U Homo sapiens cDNA clone
 IMAGE:503497 5' similar to gb:M30038 ALPHA-TRYPHASE PRECURSOR
 (HUMAN); mRNA sequence.
 ACCESSION AA131142
 VERSION AA131142.1 GI:1692796
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 639)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissole, S., Dietrich, N., Dubuque, T., Favellio, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

BASE COUNT 202 a 294 c 274 g 229 t 1 others
 Query Match 54.8%; Score 422.2; DB 13; Length 1000;

1. Not I/Dlunt end inserts were cloned into the Not I/Ecor
 V sites in the vector. EST analysis was performed on the
 unamplified library at the NIH Intramural Sequencing
 Center (NISC) "

BASE COUNT 83 a 176 c 167 g 84 t 2 others

Query Match 48.6%; Score 375; DB 12; Length 512;
 Best Local Similarity 93.5%; Pred. No. 2,6e-69;
 Matches 390; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 17 GAATGTCGGGGGTCAGGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
 Db 96 GTATGTCGGGGGTCAGGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 155
 QY 77 TCCAGGGCCCATPACTGGATGACATTTGGGGGGTCCCTCATCCACCCCGAGTGGGTGC 136
 Db 156 TCCGGACCGATPACTGGATGACATTTGGGGGGTCCCTCATCCACCCCGAGTGGGTGC 215
 QY 137 TGACCCCGCCGCGTGGGACCCGACGTCAGAGATCTGCCCCCTCAGGTGCAAC 196
 Db 216 TGACCCCGCCGCGTGGGACCCGACGTCAGAGATCTGCCCCCTCAGGTGCAAC 275
 QY 197 TCGGGGAGCAGCAGCCTTACTTACAGAGACAGCTGCTGCGGGTCAAGATCATCTGTC 256
 Db 276 TCGGGGAGCAGCAGCCTTACTTACAGAGACAGCTGCTGCGGGTCAAGATCATCTGTC 335
 QY 257 ACCCAGATTTACACCGCCGAGATTCGGAGGGGACATGCCCCCTGGAGTGGAGAGGC 316
 Db 336 ACCCAGATTTACACCGCCGAGATTCGGAGGGGACATGCCCCCTGGAGTGGAGAGGC 395
 QY 317 CGGTGAAGGTCCTCAGCCAGCAGCAGCTGACCCCTGCCCTCAGAGACCTTCC 376
 Db 396 CGGTGAAGGTCCTCAGCCAGCAGCAGCTGACCCCTGCCCTCAGAGACCTTCC 455
 QY 377 CCCCCGGGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
 Db 456 CCCCCGGGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 512

RESULT 11
 BM991728/c 693 bp mRNA linear EST 17-JUN-2002
 LOCUS UI-H-DP1-auk-a-06-0-UI.s1 NCI_CGAP_DFI Homo sapiens cDNA clone
 DEFINITION IMAGE:5870477 3', mRNA sequence.
 ACCESSION BM991728
 VERSION BM991728.1 GI:19711117
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NCI-CGAP htcp://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINt at: http://image.lnl.gov
 Seq primer: M13 FORWARD
 POLY-A=Yes

FEATURES
 source location/Qualifiers
 1..693 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5870477"
 /clone_lib="NCI_CGAP_DFI"

/tissue_type="Subchondral Bone"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Bone; Vector: p773-Pac (Pharmacia) with a
 modified polylinker; Site_1: Ecor I; Site_2: Not I;
 NCI_CGAP_DFI is a normalized cDNA library containing the
 following tissue(s): Subchondral Bone. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-805, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an Ecor I
 adaptor, digested with Not I, and cloned directionally
 into p773-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dtd)18 tail. The sequence tag for this library is
 GTTAAGGTC.
 TAG_LIB=UI-H-DP1
 TAG_TISSUE="subchondral bone"
 TAG_SEQ="GTTAAGGTC"

BASE COUNT 131 a 179 c 241 g 140 t 2 others

Query Match 45.5%; Score 351; DB 14; Length 693;
 Best Local Similarity 96.7%; Pred. No. 3.3e-64;
 Matches 357; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 395 GGGTCACCTGGTGGGGGATGTGGACAATGATGAGGGCCCTCCACCGGCATTTCCCTGCA 454
 Db 693 GGGTCACCTGGTGGGGGATGTGGACAATGATGAGGGCCCTCCACCGGCATTTCCCTGCA 634
 QY 455 AGCAGGTGAAGGTCCTCCATTAATGGAACACACATTTGTGAGCCAAATATCCACTTGGCC 514
 Db 633 AGCAGGTGAAGGTCCTCCATTAATGGAACACACATTTGTGAGCCAAATATCCACTTGGCC 574
 QY 515 CCTACACGGGAGACAGAGCTCCGCAATCGTCCGTGACGACATGCTGTGTCGGGAAACACC 574
 Db 573 CCTACACGGGAGACAGAGCTCCGCAATCGTCCGTGACGACATGCTGTGTCGGGAAACACC 514
 QY 575 GGAGGGACCTCATGGCCAGGGGGGACTCCGGAGGGCCCGTGGTGGCAAGTGAATGGACACT 634
 Db 513 GGAGGGACCTCATGGCCAGGGGGGACTCCGGAGGGCCCGTGGTGGCAAGTGAATGGACACT 454
 QY 635 GGCTGCAAGGGCCGGTGGTCACTGCTGGGCGAGAGGCTGTGCCACAGCCCGCTGGCA 694
 Db 453 GGCTGCAAGGGCCGGTGGTCACTGCTGGGCGAGAGGCTGTGCCACAGCCCGCTGGCA 394
 QY 695 TCTACACCCGTTGTCACCTACTTGTGGACTGGATCCACCACTATGTCCCAAAAAGCCCT 754
 Db 393 TCTACACCCGTTGTCACCTACTTGTGGACTGGATCCACCACTATGTCCCAAAAAGCCCT 334
 QY 755 GAAGGGGCC 763
 Db 333 GAGTCAAGGC 325

RESULT 12
 BF850308/c 376 bp mRNA linear EST 16-JAN-2001
 LOCUS BF850308
 DEFINITION C43-EN0077-181100-489-e06 EN0077 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF850308
 VERSION BF850308.1 GI:12237470
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 376)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

TITLE Simpson A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?LI=CM3&t2=CM3-EN0077-181100-489-e06&t3=2000-11-18&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 28
 High quality sequence stop: 376.

FEATURES
 source Location/Qualifiers
 1..376
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="EN0077"
 /dev_stage="Adult"
 /note="Organ: Lung_normal; Vector: puc18; Site_1: Smat. Site_2: Smat; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 62 a 115 c 121 g 78 t
 ORIGIN
 Query Match 45.4%; Score 350.2; DB 12; Length 376;
 Best Local Similarity 96.5%; Pred. No. 4.1e-64;
 Matches 358; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 144 CGCGCGTTCGCTGGGAGCAGGAGCTGAGGAGTGGCCCGCTCAAGGGTGCACACTCGCGGA 203
 Db 375 CGCGTTCAGCGGAGCGGAGCGTCAAGGATCTGCAGGCGCTCAAGGGTGCACACTCGCGGA 316
 QY 204 GCAGACCTGACTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 263
 Db 315 GCAGACCTGACTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 256
 QY 264 GTTCTACACCGCCGACATGCGAGCGAGCATGCGCTGCGTGGAGCTGGAGAGCGCGGTGA 323
 Db 255 GTTCCACACCGCCGACATGCGAGCGAGCATGCGCTGCGTGGAGCTGGAGAGCGCGGTGA 196
 QY 324 GGTCTCCACCGCCGACATGCGAGCGAGCATGCGCTGCGTGGAGCTGGAGAGCGCGGTGA 383
 Db 195 GGTCTCCACCGCCGACATGCGAGCGAGCATGCGCTGCGTGGAGCTGGAGAGCGCGGTGA 136
 QY 384 GATGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 443
 Db 135 GATGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 76
 QY 444 ATTTCCTGTGAAGCAGTGAAGTCCCATTAATGAAAACCACATTTGTGACGCAAAAATA 503
 Db 75 ATTTCCTGTGAAGCAGTGAAGTCCCATTAATGAAAACCACATTTGTGACGCAAAAAGC 16
 QY 504 CCACCTGGCG 514
 Db 15 GCACATTAAGTG 5

RESULT 13
 BM989945/c 692 bp mRNA linear EST 17-JUN-2002
 LOCUS BM989945
 DEFINITION UI-H-D10-ato-m-22-0-ui.s1_NCI_CGAP_D10 Homo sapiens cDNA clone

ACCESSION IMAGE:5862333 3', mRNA sequence.
 VERSION BM989945
 KEYWORDS BM989945.1 GI:19709334
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE NCI_CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 UNPUBLISHED (1997)
 JOURNAL Contract: Robert Strausberg, Ph.D.
 COMMENT Email: cgapb@remail.nih.gov
 Tissue procurement: Dr. Jose Mercuende
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source Location/Qualifiers
 1..692
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5862333"
 /clone_lib="NCI_CGAP_D10"
 /tissue_type="Lung Focal Fibrosis"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_D10 is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is ATAGCGCGTC.
 TAG_LIB="UI-H-D10
 TAG_ISSUE="Lung with fibrosis
 TAG_SEQ="ATAGCGCGTC"

BASE COUNT 130 a 182 c 242 g 137 t 1 others
 ORIGIN
 Query Match 45.3%; Score 349.6; DB 14; Length 692;
 Best Local Similarity 98.4%; Pred. No. 6.5e-64;
 Matches 363; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 395 GGGTACCTGGCTGGGGCCATGTGAGCAATGATGAGCGCTCCACCGCATTTCTCTGCA 454
 Db 692 GGGTACCTGGCTGGGGCCATGTGAGCAATGATGAGCGCTCCACCGCATTTCTCTGCA 633
 QY 455 ASCAGGTGAAGTCCCATTAATGAAAACCACATTTGTGAGCAAAAATACACCTTTGGGG 514
 Db 632 ACAGGTGAA-GTCCCATTAATGAAAACCACATTTGTGAGCAAAAATACACCTTTGGGG 574
 QY 574 CCTACACGGAGACGACGATCCCATTCCTGGTGGAGACATGCTGTGTGCGCGGAACACC 574
 Db 573 CMTACACGGAGACGACGATCCCATTCCTGGTGGAGACATGCTGTGTGCGCGGAACACC 514
 QY 575 GGAGGACTCATGCCAGGGCCACTCCGGAGGGCCCTGGTGTGCAAGGTGACCT 634
 Db 513 GGAGGACTCATGCCAGGGCCACTCCGGAGGGCCCTGGTGTGCAAGGTGACCT 454
 QY 635 GCCTGCAGGCGGGCGTGTGACCTGGGGCAGAGGCGTGTGCCAGGCCAACCAGCGCTGGCA 694

Db 453 GGTCTCAGGCGGGCGTGTGACAGCTGGGGGAGGGGCTGTGCCAGCCCAACCGGCTGGGA 394
 OY 695 TCTACACCGGTGTACACTTGTGACATGTGATCCACACTATGTCCCAAAAAGCCGT 754
 Db 393 TCTACACCGGTGTACACTTGTGACATGTGATCCACACTATGTCCCAAAAAGCCGT 334
 OY 755 GAAGCGGCC 763
 Db 333 GAGTCAGGC 325

RESULT 14
 B0003361/6 688 bp mRNA linear EST 26-MAR-2002
 LOCUS UI-H-E11-g2d-d-03-0-UI-s1 NCI_CGAP_E11 Homo sapiens cDNA clone
 DEFINITION IMAGE:5847122 3', mRNA sequence.
 ACCESSION B0003361
 VERSION B0003361.1 GI:19728261
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 688)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source Location/Qualifiers
 1..688
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5847122"
 /clone_lib="NCI_CGAP_E11"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
 ACACCTGCAC.
 TAG_Lib=UI-H-E11
 TAG_Tissue=chondrosarcoma
 TAG_Seq=ACACCTGCAC"

BASE COUNT 130 a 176 c 242 g 140 t
 ORIGIN
 Query Match 45.1%; Score 348; DB 14; Length 688;
 Best Local Similarity 97.3%; Pred. No. 1,4e-63;
 Matches 354; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 OY 400 ACTGGCTGGGGCGAACAATGATGAGCGCCCTCCACCGCCATTTCTCTGAAGCAG 459

Db 688 ACTGGCTGGGGCGAACAATGATGAGCGCCCTCCACCGCCATTTCTCTGAAGCAG 629
 OY 460 GTGAAGTCCCATATGGAANAACACATTTGTGACGCAAAAATACACCTTGGCCCTAC 519
 Db 628 GTGAAGTCCCATATGGAANAACACATTTGTGACGCAAAAATACACCTTGGCCCTAC 569
 OY 520 ACGGAGACGACGTCGCCGATCGCTGTCGACGACATGCTGTGCGGGGAACCGCGAG 579
 Db 568 ACGGAGACGACGTCGCCGATCGCTGTCGACGACATGCTGTGCGGGGAACCGCGAG 509
 OY 580 GACTCATGCGAGGGGACCTCCGGAGGGCCCGTGGTGTGAAGTGAATGGACCTGGCGM 639
 Db 508 GACTCATGCGAGGGGACCTCCGGAGGGCCCGTGGTGTGAAGTGAATGGACCTGGCGM 449
 OY 640 CAGGGGGGGGTGTGACGTCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 699
 Db 448 CAGGGGGGGGTGTGACGTCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 389
 OY 700 ACCCGTGTACCTACTTGTGATCCACACATATGTCCCAAAAAGCGCTGAAGC 759
 Db 388 ACCCGTGTACCTACTTGTGATCCACACATATGTCCCAAAAAGCGCTGAAGC 329
 OY 760 GGCC 763
 Db 328 AGGC 325

RESULT 15
 B3359130/c 371 bp mRNA linear EST 22-NOV-2000
 LOCUS QV3-ET0063-090800-291-f02 ET0063 Homo sapiens cDNA, mRNA sequence.
 DEFINITION B3359130
 ACCESSION B3359130.1 GI:11318202
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 371)
 AUTHORS Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 LABORATORY: Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?fl=QV3&t2=QV3-ET0063-090800-291-f02&t3=2000-08-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 12
 High quality sequence stop: 369.

FEATURES
 source Location/Qualifiers
 1..371
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0063"
 /dev_stage="Adult"
 /note="Organ: Lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products

BASE COUNT 130 a 176 c 242 g 140 t
 ORIGIN
 Query Match 45.1%; Score 348; DB 14; Length 688;
 Best Local Similarity 97.3%; Pred. No. 1,4e-63;
 Matches 354; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 OY 400 ACTGGCTGGGGCGAACAATGATGAGCGCCCTCCACCGCCATTTCTCTGAAGCAG 459

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

BASE COUNT 63 a 116 c 119 g 73 t
ORIGIN

Query Match 43.3%; Score 334.2; DB 12; Length 371;
Best Local Similarity 96.3%; Pred. No. 9.8e-61;
Matches 342; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 348 CACCCCTGCCCTGCTCCATGAGACCTTCCCGGGGATGCCGTTGGTGCACCTGCGCTG 407
 || |||||
 Db 371 CATGCTGCCCTGCTCCGAGACCTTCCCGGGGATGCCGTTGGTGCACCTGCGCTG 312

OY 408 GGGCGATGTGACAAATGATGAGCCCTCCACCGCCATTTCTCTGAAGCAGGTGAAGGT 467
 |||||
 Db 311 GGGCGATGTGACAAATGATGAGCCCTCCACCGCCATTTCTCTGAAGCAGGTGAAGGT 252

OY 468 CCCGATAATGGAAAAACCAATTTGTGAGCAAAAATACCACTTGGCGGCTACCGGGAGA 527
 |||||
 Db 251 CCCGATAATGGAAAAACCAATTTGTGAGCAAAAATACCACTTGGCGGCTACCGGGAGA 192

OY 528 CGACGTCGCCATGCTCCGTGACGACATGCTGTGTGCGGGAACCCCGAGGGACTCATG 587
 |||||
 Db 191 CGACGTCGCCATGCTCCGTGAGACATGCTGTGTGCGGGAACCCCGAGGGACTCATG 132

OY 588 CCAAGGGGACTCCGGAGGGCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCACGGGG 647
 |||||
 Db 131 CAAAGGGGACTCCGGAGGGCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCACGGGG 72

OY 648 GGTGGTCAAGCTGGGGCGAGGGCTGTGCCCAACCGGCTGGGCAATCTACACC 702
 |||||
 Db 71 GGTGGTCAAGCTGGGGCGAGGGCTGTGCCCAACCGGCTGGGCAATCTACACC 17

Search completed: January 31, 2003, 06:50:06
Job time : 2242 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: January 31, 2003, 03:49:17 ; Search time 264 Seconds
(without alignments)
6576.859 Million cell updates/sec

Title: US-09-598-982-20
Perfect score: 771
Sequence: 1 gggccctcgcgagaagaat.....cgtgaagcggccgcgctcgt 771

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771	100.0	771	24 AAS20775	DNA encoding human
2	769.4	99.8	771	24 AAS20783	DNA encoding human
3	764.6	99.2	771	21 AAZ40175	Human beta-tryptas
4	764.6	99.2	771	24 AAS20765	DNA encoding recom
5	763	99.0	771	24 AAS20763	DNA encoding human
6	761.4	98.8	771	24 AAS20776	DNA encoding human
7	759.8	98.5	771	24 AAS20784	DNA encoding human
8	755	97.9	771	24 AAS20777	DNA encoding human
9	755	97.9	771	24 AAS20778	DNA encoding human

10	753.4	97.7	771	24 AAS20785	DNA encoding human
11	753.4	97.7	771	24 AAS20786	DNA encoding human
12	735	95.3	735	24 AAS20779	DNA encoding human
13	733.4	95.1	735	24 AAS20787	DNA encoding human
14	731	94.8	731	19 AAS44330	Human mast cell tr
15	731	94.8	731	19 AAV44329	Human mast cell tr
16	731	94.8	731	19 AAV44329	Human mast cell tr
17	731	94.8	731	19 AAV42711	Human mast cell tr
18	731	94.8	731	21 AAF21079	Human low adenosin
19	731	94.8	731	21 AAF21079	Human low adenosin
20	731	94.8	731	21 AAF21077	Human low adenosin
21	731	94.8	731	21 AAF21078	Human low adenosin
22	731	94.8	731	21 AAF21078	Human low adenosin
23	731	94.8	731	21 AAF21078	Human low adenosin
24	731	94.8	731	21 AAF21078	Human low adenosin
25	731	94.8	731	21 AAF21078	Human low adenosin
26	728.6	94.5	735	21 AAZ40172	DNA encoding recom
27	728.6	94.5	735	24 AAS20766	DNA encoding human
28	727	94.3	735	24 AAS20760	DNA encoding human
29	726.2	94.2	1081	19 AAV44331	Human mast cell tr
30	726.2	94.2	1081	19 AAV42713	Human mast cell tr
31	726.2	94.2	1081	21 AAF21082	Human low adenosin
32	726.2	94.2	1081	21 AAF21082	Human low adenosin
33	726.2	94.2	1081	24 ABL64532	Human benign prost
34	726.2	94.2	1081	24 ABL61818	Colon adenocarcino
35	726.2	94.2	1081	24 ABL62377	Colon adenocarcino
36	726.2	94.2	1081	24 ABL66816	Lung cancer relate
37	726.2	94.2	1081	24 ABL66816	Lung cancer relate
38	725.4	94.1	735	24 AAS20780	DNA encoding human
39	723.8	93.9	735	24 AAS20788	DNA encoding human
40	719	93.3	735	24 AAS20781	DNA encoding human
41	719	93.3	735	24 AAS20782	DNA encoding human
42	719	93.3	1221	20 AAZ41376	Human normal uteru
43	718.2	93.2	2662	24 AAD23854	Human protease PRT
44	717.4	93.0	735	24 AAS20789	DNA encoding human
45	717.4	93.0	735	24 AAS20790	DNA encoding human

ALIGNMENTS

RESULT 1
AAS20775 standard: DNA; 771 BP.
ID AAS20775
AC AAS20775;
DT 09-APR-2002 (first entry)
DX
DE DNA encoding human beta-II tryptase active site mutant H44A #1.
KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutant; ds.
OS Homo sapiens.
OS Synthetic.
XX WO200198470-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US19681.
XX
XX 21-JUN-2000; 2000US-0598982.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Maffit M, Niles AL, Haak-Frendscho M;
XX WPI; 2002-114578/15.
XX P-PSDB; AAU12009.
XX
XX DNA construct for producing enzymatically-inactive proteolytic

Db 421 AATGATGAGCCCTCCACCCGATTTCTGTAAGCAGTGAAGTCCCATTAATATGGA 480
 Qy 481 AACCCATTGTTGAGCGCAAAATPACACCTTGCGCCCTFACAGCGGAGACGATCCGATC 540
 Db 481 AACCCATTGTTGAGCGCAAAATPACACCTTGCGCCCTFACAGCGGAGACGATCCGATC 540
 Qy 541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGAGGAGACTATGCCAGGCGACTCC 600
 Db 541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGAGGAGACTATGCCAGGCGACTCC 600
 Qy 601 GGAGGGCCCTGTGTGTGCAAGTGAATGGACACTGGCTGCAAGCGCGGCTGACGCTGG 660
 Db 601 GGAGGGCCCTGTGTGTGCAAGTGAATGGACACTGGCTGCAAGCGCGGCTGACGCTGG 660
 Qy 661 GGCGAGGCTGTGGCCACGACCCAGCGCCCTGACATCTACACCCGCTGTACTACTTTG 720
 Db 661 GGCGAGGCTGTGGCCACGACCCAGCGCCCTGACATCTACACCCGCTGTACTACTTTG 720
 Qy 721 GACTGGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGCCCGCTGCT 771
 Db 721 GACTGGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGCCCGCTGCT 771
 RESULT 4
 AAS20765
 ID AAS20765 standard; DNA; 771 BP.
 AC AAS20765;
 XX
 AC AAS20765;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding recombinant human beta-II tryptase.
 XX
 KW Human: proteolytic tryptase; protease; recombinant beta-II tryptase;
 KM enzyme: gene; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 7..756
 FT /*tag= a
 FT /partial
 FT /product= "Recombinant beta-II tryptase"
 FT /note= "This sequence lacks a start codon"
 XX
 PN MO200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 PE 20-JUN-2001; 2001WO-US19681.
 PF 21-JUN-2000; 2000US-0598982.
 PR
 XX
 PA (PROM-) PROMEGA CORP.
 PI Maffitt M, Niles AL, Haak-Frendscho M;
 DR WPI: 2002-114578/15.
 DR P-PSDB; AAU12007.
 XX
 XX DNA construct for producing enzymatically-inactive proteolytic
 PT tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PT an active site mutation
 XX
 PS Claim 43; Page 75-77; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives

CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modeling studies. The
 CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. The present sequence encodes for recombinant
 CC human beta-II tryptase.
 CC
 XX
 XX Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 other.
 Query Match 99.2% Score 764.6; DB 24; Length 771;
 Best Local Similarity 99.5%; Pred. No. 5e-147;
 Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GGGCCCTCGAGAAAAGATGTCGGGGTCAAGAGGCCCCAGAGCAATGGCCCTG 60
 Db 1 GGGCCCTCGAGAAAAGATGTCGGGGTCAAGAGGCCCCAGAGCAATGGCCCTG 60
 Qy 61 CAGTGAAGCTGAGAGTCCACGCGCCATPACTGATGCACTTGTGGGGCTCCCTATC 120
 Db 61 CAGTGAAGCTGAGAGTCCACGCGCCATPACTGATGCACTTGTGGGGCTCCCTATC 120
 Qy 121 CACCCCGAGTGGTGTGTCAGCGCGCGCGTGGGGAGGAGCGATGATCTGGCC 180
 Db 121 CACCCCGAGTGGTGTGTCAGCGCGCGCGTGGGGAGGAGCGATGATCTGGCC 180
 Qy 181 GCGCTCAGAGGTGCAACTGCGGGAGGAGCAGCCCTTACCTACACAGAGCAACTGCTCCGGT 240
 Db 181 GCGCTCAGAGGTGCAACTGCGGGAGGAGCAGCCCTTACCTACACAGAGCAACTGCTCCGGT 240
 Qy 241 AGCAGGATCAGTGTGACCCCAAGTCTTACACCGCCAGATGGAGCGGATGCGCTG 300
 Db 241 AGCAGGATCAGTGTGACCCCAAGTCTTACACCGCCAGATGGAGCGGATGCGCTG 300
 Qy 301 CTGGAGCTGGAAGAGCGGAGTGTCCAGCCAGCCAGCGTCCAGCGGATCCCTG 360
 Db 301 CTGGAGCTGGAAGAGCGGAGTGTCCAGCCAGCCAGCGTCCAGCGGATCCCTG 360
 Qy 361 GCTCAGAGACCTTCCCGCCCGGGAGTGGCTGTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Db 361 GCTCAGAGACCTTCCCGCCCGGGAGTGGCTGTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Qy 421 AATGATGAGCGCTCCACCGCCATTTCTGTGAAGCAGTGAAGTCCCATATATGGA 480
 Db 421 AATGATGAGCGCTCCACCGCCATTTCTGTGAAGCAGTGAAGTCCCATATATGGA 480
 Qy 481 AACCCATTGTTGAGCGCAAAATPACACCTTGCGCCCTFACAGCGGAGACGATCCGATC 540
 Db 481 AACCCATTGTTGAGCGCAAAATPACACCTTGCGCCCTFACAGCGGAGACGATCCGATC 540
 Qy 541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGAGGAGACTATGCCAGGCGACTCC 600
 Db 541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGAGGAGACTATGCCAGGCGACTCC 600
 Qy 601 GGAGGGCCCTGTGTGTGCAAGTGAATGGACACTGGCTGCAAGCGCGGCTGACGCTGG 660
 Db 601 GGAGGGCCCTGTGTGTGCAAGTGAATGGACACTGGCTGCAAGCGCGGCTGACGCTGG 660
 Qy 661 GGCGAGGCTGTGGCCACGACCCAGCGCCCTGACATCTACACCCGCTGTACTACTTTG 720
 Db 661 GGCGAGGCTGTGGCCACGACCCAGCGCCCTGACATCTACACCCGCTGTACTACTTTG 720
 Qy 721 GACTGGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGCCCGCTGCT 771
 Db 721 GACTGGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGCCCGCTGCT 771
 RESULT 5
 AAS20763

ID AAS20763 standard; DNA: 771 BP.
 AC AAS20763;
 XX
 DM 09-APR-2002 (first entry)
 DE DNA encoding human beta-I tryptase.
 XX
 KW Human: proteolytic tryptase; protease; beta-I tryptase;
 KW enzyme; gene; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 7.-756 /tag= a
 FT /partial /product= "Beta-I tryptase"
 FT /note= "This sequence lacks a start codon"
 FT
 XX
 PN MO200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-US19681.
 PR 21-JUN-2000; 2000US-0598982.
 PA (PROM-) PROMEGA CORP.
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX
 DR MPI: 2002-114578/15.
 DR P-PSDB: AAU12006.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT tryptase, comprises DNA sequence encoding proteolytic tryptase having
 PT an active site mutation -
 XX
 PS Disclosure: Page 72-74; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modeling studies. The
 CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. The present sequence encodes for human
 CC beta-I tryptase.
 CC
 XX
 SO Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 other;
 Query Match 99.0%; Score 763; DB 24; Length 771;
 Best Local Similarity 99.4%; Pred. No. 1,1e-146;
 Matches 766; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 GGGCCCTCGAGAAAAAAGATCGTGGGGGTCAAGAGCCGCCAGAGCAAGTGGCCCTGG 60
 DB 1 GGGCCCTCGAGAAAAAAGATCGTGGGGGTCAAGAGCCGCCAGAGCAAGTGGCCCTGG 60
 OY 61 CAGGTGAGCCTGAGGATCGCCAGCCATATCTGATGATGATGATGATGATGATGATGATGAT 120
 DB 61 CAGGTGAGCCTGAGGATCGCCAGCCATATCTGATGATGATGATGATGATGATGATGATGAT 120

OY 121 CACCCCGAGTGGTCTGTACCGCCGGCGTGGGAGCCGAGCAGATCTGGCC 180
 DB 121 CACCCCGAGTGGTCTGTACCGCCGGCGTGGGAGCCGAGCAGATCTGGCC 180
 OY 181 GCCCTCAGGTTCAACCTCGGGGAGGAGCACTCTACTACAGAGCCAGCTGCCGGGTC 240
 DB 181 GCCCTCAGGTTCAACCTCGGGGAGGAGCACTCTACTACAGAGCCAGCTGCCGGGTC 240
 OY 241 AGCAGATATCTGTACCCACCACAGTTCATACACCCGCCAGATGGAGGAGCAATGCCCTG 300
 DB 241 AGCAGATATCTGTACCCACCACAGTTCATACACCCGCCAGATGGAGGAGCAATGCCCTG 300
 OY 301 CTGAGCTGAGAGAGCCGGTGAAGGTCTCCAGCCACGTCACAGCGTACCCCTGCCCCCT 360
 DB 301 CTGAGCTGAGAGAGCCGGTGAAGGTCTCCAGCCACGTCACAGCGTACCCCTGCCCCCT 360
 OY 361 GCCTCAGAGACCTTCCCCCGGGGATGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420
 DB 361 GCCTCAGAGACCTTCCCCCGGGGATGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420
 OY 421 AATGATGAGCCCTCCACCCGATTTCTCTGAAAGCAGGTGAAGTCCCATATGGAA 480
 DB 421 AATGATGAGCCCTCCACCCGATTTCTCTGAAAGCAGGTGAAGTCCCATATGGAA 480
 OY 481 AACCAATTTGAGCAGCAAAATACCACCTTGGGCGCTACACGAGAGAGCAGCAGCTCCGCAATC 540
 DB 481 AACCAATTTGAGCAGCAAAATACCACCTTGGGCGCTACACGAGAGAGCAGCAGCTCCGCAATC 540
 OY 541 GTCCGTGAGCAGCAGTCTGTGTCGGGAAACACCCGGAGGAGCAGTGCAGGGCCAGATCC 600
 DB 541 GTCCGTGAGCAGCAGTCTGTGTCGGGAAACACCCGGAGGAGCAGTGCAGGGCCAGATCC 600
 OY 601 GGAGGGCCCCGTGGTGTGCAAGGTGAATGGCACTGGTGTGCAAGGGGGGTGCTAGCTGG 660
 DB 601 GGAGGGCCCCGTGGTGTGCAAGGTGAATGGCACTGGTGTGCAAGGGGGGTGCTAGCTGG 660
 OY 661 GGCGAGGGCTGTGCCACAGCCCAACCGCCTGSGCATCTACACCCTGATCACTACTTTG 720
 DB 661 GGCGAGGGCTGTGCCACAGCCCAACCGCCTGSGCATCTACACCCTGATCACTACTTTG 720
 OY 721 GACTGGATCCACCACTATGTCGCCAAAAAAGCCGTGAAGCGGCCGCTGCT 771
 DB 721 GACTGGATCCACCACTATGTCGCCAAAAAAGCCGTGAAGCGGCCGCTGCT 771
 RESULT 6
 AAS20776
 ID AAS20776 standard; DNA: 771 BP.
 AC AAS20776;
 XX
 DM 09-APR-2002 (first entry)
 DE DNA encoding human beta-II tryptase active site mutant D91A #1.
 XX
 KW Human: proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN MO200198470-A2.
 PD 27-DEC-2001.
 PF 20-JUN-2001; 2001WO-US19681.
 PR 21-JUN-2000; 2000US-0598982.
 PA (PROM-) PROMEGA CORP.
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX

DR WP1: 2002-114578/15.
 DR P-PSDB: AAU12010.
 XX
 PR DNA construct for producing enzymatically-inactive proteolytic
 PR trypsinase, comprises DNA sequence encoding proteolytic trypsinase having
 PR an active site mutation -
 PS
 XX Claim 7: Page 86-87; 126pp; English.
 CC The present invention relates to recombinant human proteolytic
 CC trypsinases, active site mutants of these trypsinases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsinase with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsinase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II trypsinase. The active site mutants of proteolytic trypsinase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypsinase produced are
 CC useful as an antigen to generate anti-human trypsinase antibodies
 CC and in drug screening for compounds which act as trypsinase inhibitors,
 CC antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 CC human beta-II trypsinase active site mutants.
 XX
 XX Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 other;

Query Match 98.8%; Score 761.4; DB 24; Length 771;
 Best Local Similarity 99.1%; Pred. No. 2.2e-146;
 Matches 765; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGCCCCCTCGAAGAAAGATGTCGGGGGTGTCAGAGAGGCCCCCAGAGAGCAAGTGGCCCTGG 60
 DB 1 GGGCCCCCTCGAAGAAAGATGTCGGGGGTGTCAGAGAGGCCCCCAGAGAGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCCTGAGAGATCCAGCCCAATGATGATGATGATGATGATGATGATGATGATGATG 120
 DB 61 CAGGTGAGCCTGAGAGATCCAGCCCAATGATGATGATGATGATGATGATGATGATGATGATG 120
 QY 121 CACCCCACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 DB 121 CACCCCACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 QY 181 GGCCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 181 GGCCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 QY 241 AGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 AGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 CTGAGAGCTGAG 360
 DB 301 CTGAGAGCTGAG 360
 QY 361 GGCCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 DB 361 GGCCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 421 AATG 480
 DB 421 AATG 480
 QY 481 AACCCACATTTGTGAGCAAAATAACCACTTGTGGCCCTACACGGGAGAGACAGAGCTCCGCAATC 540
 DB 481 AACCCACATTTGTGAGCAAAATAACCACTTGTGGCCCTACACGGGAGAGACAGAGCTCCGCAATC 540
 QY 541 GTCCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 DB 541 GTCCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 601 GGAGGCCCCCTGAG 660
 DB 601 GGAGGCCCCCTGAG 660
 QY 661 GGGAGAGGCTGTGAG 720
 DB 661 GGGAGAGGCTGTGAG 720
 QY 721 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
 DB 721 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
 RESULT 7
 AAS20784
 ID AAS20784 standard; DNA; 771 BP.
 AC AAS20784;
 XX
 XX 09-APR-2002 (first entry)
 DR
 XX
 DE DNA encoding human beta-II trypsinase active site mutant D91A #3.
 XX
 KW Human; proteolytic trypsinase; protease; recombinant beta-II trypsinase;
 KW enzyme; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200198470-A2.
 PD 27-DEC-2001.
 PF 20-JUN-2001; 2001WO-0519681.
 XX
 XX 21-JUN-2000; 2000US-0598982.
 PR
 XX
 PA (PROM-) PROMEGA CORP.
 PA
 PI Maffit M, Niles AL, Haak-Frendscho M;
 DR
 DR WP1: 2002-114578/15.
 DR P-PSDB: AAU12018.
 XX
 XX
 PR DNA construct for producing enzymatically-inactive proteolytic
 PR trypsinase, comprises DNA sequence encoding proteolytic trypsinase having
 PR an active site mutation -
 PS
 XX Claim 7: Page 107-109; 126pp; English.

The present invention relates to recombinant human proteolytic
 trypsinases, active site mutants of these trypsinases and the methods for
 producing these. The method involves the production of a DNA expression
 construct comprising a promoter operably linked to a secretion signal
 sequence which is operably linked to a DNA sequence encoding a
 proteolytic trypsinase with an active site mutation (the construct drives
 expression of a mature proteolytic trypsinase that lacks enzymatic activity
 due to the active site mutation, in hosts transformed to contain the
 construct). The method is useful for producing enzymatically-active
 beta-II trypsinase. The active site mutants of proteolytic trypsinase provide
 a tool to investigate the structural and functional properties of the
 protease and its enzymatic activity, and for modelling studies. The
 enzymatically-active, recombinant proteolytic trypsinase produced are
 useful as an antigen to generate anti-human trypsinase antibodies
 and in drug screening for compounds which act as trypsinase inhibitors,
 antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 human beta-II trypsinase active site mutants.
 Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 other;
 Query Match 98.5%; Score 759.8; DB 24; Length 771;
 Best Local Similarity 99.1%; Pred. No. 4.7e-146;
 Matches 764; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAAGAAAAGATGTCGGGGGTCAGAGAGCCCCAGAGGCAAGTGGCCCTGG 60
 |||||||
 Db 1 GGGCCCTCGAAGAAAAGATGTCGGGGGTCAGAGAGCCCCAGAGGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCCCTGAGAGATCCACGGCCCATATGATGATGACTTCTGCGGGGGCTCCCTCATC 120
 |||||||
 Db 61 CAGGTGAGCCCTGAGAGATCCACGGCCCATATGATGATGACTTCTGCGGGGGCTCCCTCATC 120
 QY 121 CACCCCGAGTGGTGTGATACCGCCCGCGGCTGCTGGGAGACCGGATCAAGATGTGGCC 180
 |||||||
 Db 121 CACCCCGAGTGGTGTGATACCGCCCGCGGCTGCTGGGAGACCGGATCAAGATGTGGCC 180
 QY 121 CACCCCGAGTGGTGTGATACCGCCCGCGGCTGCTGGGAGACCGGATCAAGATGTGGCC 180
 |||||||
 Db 121 CACCCCGAGTGGTGTGATACCGCCCGCGGCTGCTGGGAGACCGGATCAAGATGTGGCC 180
 QY 181 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 240
 |||||||
 Db 181 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 240
 QY 241 AGCAGGATCATGTCGACCCACAGTTCTACACCCCGCATCGAGATCGGACATCGCCCTG 300
 |||||||
 Db 241 AGCAGGATCATGTCGACCCACAGTTCTACACCCCGCATCGAGATCGGACATCGCCCTG 300
 QY 301 CTGGAGCTGGAGGACCGGTGAAGTCTCCACGCGTACAGCCGATCGCCCTG 360
 |||||||
 Db 301 CTGGAGCTGGAGGACCGGTGAAGTCTCCACGCGTACAGCCGATCGCCCTG 360
 QY 361 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 420
 |||||||
 Db 361 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 420
 QY 421 AATGATGAGCCCTCCACCGCCATTTCTGTAAGGAGTGAAGGTTCCCATTAATGGA 480
 |||||||
 Db 421 AATGATGAGCCCTCCACCGCCATTTCTGTAAGGAGTGAAGGTTCCCATTAATGGA 480
 QY 481 AACCCATTTGTAAGGAGTGAAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAG 540
 |||||||
 Db 481 AACCCATTTGTAAGGAGTGAAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAG 540
 QY 541 GTCCGTCGACAGCATGCTGTGTGCCGGGAACAACCCGGAGGAGTCAATGACCGGACCTCC 600
 |||||||
 Db 541 GTCCGTCGACAGCATGCTGTGTGCCGGGAACAACCCGGAGGAGTCAATGACCGGACCTCC 600
 QY 601 GGAGGGCCCTGTGTGTGCAAGGTGAATGGCACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 |||||||
 Db 601 GGAGGGCCCTGTGTGTGCAAGGTGAATGGCACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 QY 661 GCGCAGGCGCTGT 720
 |||||||
 Db 661 GCGCAGGCGCTGT 720
 QY 721 GACTGTGATCCACCACTATGTCTCCCAAAAAGCCGTGAAGCGGGCCGCTGCTGT 771
 |||||||
 Db 721 GACTGTGATCCACCACTATGTCTCCCAAAAAGCCGTGAAGCGGGCCGCTGCTGT 771
 RESULT 8
 AAS20777
 ID AAS20777 standard; DNA; 771 BP.
 AC AAS20777;
 DT 09-Apr-2002 (first entry)
 DE DNA encoding human beta-II tryptase active site mutant S194A #1.
 DE Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; ds.
 KN Homo sapiens.
 OS Synthetic.
 XX MO200198470-A2.
 XX PN 27-DEC-2001.
 XX PD

XX 20-JUN-2001; 2001WO-US19681.
 PF 21-JUN-2000; 2000US-0598982.
 PR (PROM-) PROMEGA CORP.
 PA Maffei M, Niles AL, Haak-Frendscho M;
 PI WPI: 2002-114578/15.
 DR P-PSDB; AAU12011.
 XX
 XX DNA construct for producing enzymatically-inactive proteolytic
 XX tryptase, comprises DNA sequence encoding proteolytic tryptase having
 XX an active site mutation
 XX
 XX Claim 7; Page 88-90; 126pp; English.
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-inactive
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies
 CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 CC human beta-II tryptase active site mutants.
 CC
 CC Sequence 771 BP; 150 A; 255 C; 241 G; 125 T; 0 other;
 CC XX
 XX
 XX Query Match 97.9%; Score 755; DB 24; Length 771;
 XX Best Local Similarity 98.7%; Pred. No 4.5e-145;
 XX Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 GGGCCCTCGAAGAAAAGATGTCGGGGGTCAGAGAGCCCCAGAGGCAAGTGGCCCTGG 60
 |||||||
 Db 1 GGGCCCTCGAAGAAAAGATGTCGGGGGTCAGAGAGCCCCAGAGGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCCCTGAGAGATCCACGGCCCATATGATGATGACTTCTGCGGGGGCTCCCTCATC 120
 |||||||
 Db 61 CAGGTGAGCCCTGAGAGATCCACGGCCCATATGATGATGACTTCTGCGGGGGCTCCCTCATC 120
 QY 121 CACCCCGAGTGGTGTGATACCGCCCGCGGCTGCTGGGAGACCGGATCAAGATGTGGCC 180
 |||||||
 Db 121 CACCCCGAGTGGTGTGATACCGCCCGCGGCTGCTGGGAGACCGGATCAAGATGTGGCC 180
 QY 181 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 240
 |||||||
 Db 181 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 240
 QY 241 AGCAGGATCATGTCGACCCACAGTTCTACACCCCGCATCGAGATCGGACATCGCCCTG 300
 |||||||
 Db 241 AGCAGGATCATGTCGACCCACAGTTCTACACCCCGCATCGAGATCGGACATCGCCCTG 300
 QY 301 CTGGAGCTGGAGGACCGGTGAAGTCTCCACGCGTACAGCCGATCGCCCTG 360
 |||||||
 Db 301 CTGGAGCTGGAGGACCGGTGAAGTCTCCACGCGTACAGCCGATCGCCCTG 360
 QY 361 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 420
 |||||||
 Db 361 GCGCTCAGAGGTCACACTCGGGGAGGACCACTTACCAAGGACAGCAGCTGCTGGCGGTG 420
 QY 421 AATGATGAGCCCTCCACCGCCATTTCTGTAAGGAGTGAAGGTTCCCATTAATGGA 480
 |||||||
 Db 421 AATGATGAGCCCTCCACCGCCATTTCTGTAAGGAGTGAAGGTTCCCATTAATGGA 480

OY 481 AACCAATTGTGTGACGCAAAATATACCACCTTGGCCCTACACGCGGAGACGACGCTCCGCAATC 540
 DB 481 AACCAATTGTGTGACGCAAAATATACCACCTTGGCCCTACACGCGGAGACGACGCTCCGCAATC 540
 OY 541 GTCCGTGACGACATGCTGTGTGTCCGGGAAACACCCGGAGGACTCATGCCAGGGCGCAATCC 600
 DB 541 GTCCGTGACGACATGCTGTGTGTCCGGGAAACACCCGGAGGACTCATGCCAGGGCGCAATCC 600
 OY 601 GGAGGGCCCTGTGTGGAAGGTGATGGACCTGTGCTGCACAGGGCGGCTGTGCTACGCTGG 660
 DB 601 GGAGGGCCCTGTGTGGAAGGTGATGGACCTGTGCTGCACAGGGCGGCTGTGCTACGCTGG 660
 OY 661 GGCGAGGGGCTGTGTGCCCAAGCCCAAGCCGCTGTGCTACACCCGCTGTGCTACGCTGG 720
 DB 661 GGCGAGGGGCTGTGTGCCCAAGCCCAAGCCGCTGTGCTACACCCGCTGTGCTACGCTGG 720
 OY 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGCTGAAGGGCGGCGCTGTCT 771
 DB 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGCTGAAGGGCGGCGCTGTCT 771
 RESULT 9
 AAS20778
 ID AAS20778 standard; DNA; 771 BP.
 AC AAS20778;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding human beta-II tryptase active site mutant S194A #2.
 XX
 KM Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 XX
 XX Humzyme; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-US19681.
 XX
 PR 21-JUN-2000; 2000US-0598982.
 PA (PROM-) PROMEGA CORP.
 PI Maffit M, Niles AL, Haak-Frendscho M;
 DR WPI: 2002-114578/15.
 DR P-PSDB; AAU12012.
 PS
 XX Claim 7: Page 91-92; 126pp; English.
 CC The present invention relates to recombinant human proteolytic
 CC tryptases, active site mutants of these tryptases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic tryptase with an active site mutation (the construct drives
 CC expression of a mature proteolytic tryptase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II tryptase. The active site mutants of proteolytic tryptase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic tryptase produced are
 CC useful as an antigen to generate anti-human tryptase antibodies

CC and in drug screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 CC human beta-II tryptase active site mutants.
 XX
 S0 Sequence 771 BP; 152 A; 255 C; 241 G; 123 T; 0 other:
 Query Match 97.9%; Score 755; DB 24; Length 771;
 Best Local Similarity 98.7%; Pred. No. 4.5e-145;
 Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 OY 1 GGGCCCTTCGAAAGAAATGCTGGGGGTGACGAGGGCCCCAGAGACGAACTGGCCCTGG 60
 DB 1 GGGCCCTTCGAAAGAAAGATGCTGGGGGTGACGAGGGCCCCAGAGAACTGGCCCTGG 60
 OY 61 CAGGTGAGCCTGAGAGTCCACGCGCCCATACTGATGATGACATCTTGTGGGGGCTCCCTCATC 120
 DB 61 CAGGTGAGCCTGAGAGTCCACGCGCCCATACTGATGATGACATCTTGTGGGGGCTCCCTCATC 120
 OY 121 CACCCCAAGTGGGTCTGACCGCCCGCGGCGTGGGAGCCGGAGAGATCTGGCC 180
 DB 121 CACCCCAAGTGGGTCTGACCGCCCGCGGCGTGGGAGCCGGAGAGATCTGGCC 180
 OY 181 GCCCTCAGAGGTGCAACCTGCGGGGAGCAGCACTCTACTACAGAGACCTGCTGCCGCTC 240
 DB 181 GCCCTCAGAGGTGCAACCTGCGGGGAGCAGCACTCTACTACAGAGACCTGCTGCCGCTC 240
 OY 241 AGCAGGATCATGCTGACCCACAGTCTTAACACCGCCAGANTCGAGGACGATCGCCCTG 300
 DB 241 AGCAGGATCATGCTGACCCACAGTCTTAACACCGCCAGANTCGAGGACGATCGCCCTG 300
 OY 301 CTGAGGCTGAGAGAGCCGGTGAAGGTTCACAGCCAGCTCCACAGCGGATCGCCCTC 360
 DB 301 CTGAGGCTGAGAGAGCCGGTGAAGGTTCACAGCCAGCTCCACAGCGGATCGCCCTC 360
 OY 361 GCCCTCAGAGACCTTCCCGCCCGGGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 DB 361 GCCCTCAGAGACCTTCCCGCCCGGGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 OY 421 AATGATGAGCGCCCTCCACCGCCATTTCTGTAAGCAGGTGAAGTCCCATTAATGGA 480
 DB 421 AATGATGAGCGCCCTCCACCGCCATTTCTGTAAGCAGGTGAAGTCCCATTAATGGA 480
 OY 481 AACCAATTGTGTGACGCAAAATATACCACCTTGGCCCTACACGCGGAGACGACGCTCCGCAATC 540
 DB 481 AACCAATTGTGTGACGCAAAATATACCACCTTGGCCCTACACGCGGAGACGACGCTCCGCAATC 540
 OY 541 GTCCGTGACGACATGCTGTGTGTCCGGGAAACACCCGGAGGACTCATGCCAGGGCGCAATCC 600
 DB 541 GTCCGTGACGACATGCTGTGTGTCCGGGAAACACCCGGAGGACTCATGCCAGGGAGACGCGC 600
 OY 601 GGAGGGCCCTGTGTGGAAGGTGATGGACCTGTGCTGCACAGGGCGGCTGTGCTACGCTGG 660
 DB 601 GGAGGGCCCTGTGTGGAAGGTGATGGACCTGTGCTGCACAGGGCGGCTGTGCTACGCTGG 660
 OY 661 GGCGAGGGGCTGTGTGCCCAAGCCCAAGCCGCTGTGCTACACCCGCTGTGCTACGCTGG 720
 DB 661 GGCGAGGGGCTGTGTGCCCAAGCCCAAGCCGCTGTGCTACACCCGCTGTGCTACGCTGG 720
 OY 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGCTGAAGGGCGGCGCTGTCT 771
 DB 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGCTGAAGGGCGGCGCTGTCT 771
 RESULT 10
 AAS20785
 ID AAS20785 standard; DNA; 771 BP.
 AC AAS20785;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding human beta-II tryptase active site mutant S194A #5.
 XX

KW Human; proteolytic trypsin; protease; recombinant beta-II trypsin;
 KW enzyme; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 XX MO200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US19681.
 XX 21-JUN-2000; 2000US-0598982.
 PA (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 DR WPI: 2002-114578/15.
 DR P-PSDB: AAU12019.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT trypsin, comprises DNA sequence encoding proteolytic trypsin having
 PT an active site mutation -
 XX
 XX Claim 7; Page 110-111; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic
 CC trypsin, active site mutants of these trypsin and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsin with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsin that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II trypsin. The active site mutants of proteolytic trypsin provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypsin produced are
 CC useful as an antigen to generate anti-human trypsin antibodies
 CC and in drug screening for compounds which act as trypsin inhibitors,
 CC antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 CC human beta-II trypsin active site mutants.
 CC
 XX
 XX Sequence 771 BP; 150 A; 256 C; 240 G; 125 T; 0 other;

Query Match 97.7%; Score 753.4; DB 24; Length 771;
 Best Local Similarity 98.6%; Pred. No. 9.6e-145;
 Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGCCCCCGGAAAAAGATGCTGGGGGTGAGAGAGCCCGCCAGAGCAAGTGGCCCTGG 60
 Db 1 GGGCCCCCGGAAAAAGATGCTGGGGGTGAGAGAGCCCGCCAGAGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCTGAGAGTCCACGGCCCATCTGATGATGACTCTTCTGGGGGGCTCCCTCATC 120
 Db 61 CAGGTGAGCTGAGAGTCCACGGCCCATCTGATGATGACTCTTCTGGGGGGCTCCCTCATC 120
 QY 121 CACCCCGAGTGGTGTGACCGCCGCGTGCCTGGGAGCCGGACGCTCAAGATCTGGCC 180
 Db 121 CACCCCGAGTGGTGTGACCGCCGCGTGCCTGGGAGCCGGACGCTCAAGATCTGGCC 180
 QY 181 GCCCTCAGAGGTGCAACCTGGGGAGAGCACTTACTACTACAGAGCAAGTGGCCGCTC 240
 Db 181 GCCCTCAGAGGTGCAACCTGGGGAGAGCACTTACTACTACAGAGCAAGTGGCCGCTC 240
 QY 241 AGCAGATCATCTGTCACCCACAGTCTTACACCGCCGCAAGTGGAGACATGGCCCGC 300
 Db 241 AGCAGATCATCTGTCACCCACAGTCTTACACCGCCGCAAGTGGAGACATGGCCCGC 300
 QY 301 CTGAGCTGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACCGCTGACCCCTGCC 360
 Db 301 CTGAGCTGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACCGCTGACCCCTGCC 360

Db 301 CTGAGCTGAGAGACCCGGTGAAGGTCTCCAGCCAGCTCCACACCGCTGACCCCTGCC 360
 QY 361 GCGTCAGAGACTTCCCGCGGGGATGCGGTGGGTCAGTGGGTCAGTGGGATGTGGAC 420
 Db 361 GCGTCAGAGACTTCCCGCGGGGATGCGGTGGGTCAGTGGGTCAGTGGGATGTGGAC 420
 QY 421 AATGATGAGCCCTCCACCCGCAATTTCTGTAAGAGTGAAGTGGCCATTAATGGAA 480
 Db 421 AATGATGAGCCCTCCACCCGCAATTTCTGTAAGAGTGAAGTGGCCATTAATGGAA 480
 QY 481 AACCAATTTGTGAGCAAAATAATACCACTTGGCGCTTACAGGGAGAGCAAGTGGC 540
 Db 481 AACCAATTTGTGAGCAAAATAATACCACTTGGCGCTTACAGGGAGAGCAAGTGGC 540
 QY 541 GTCCCTGACAGCAATGCTGTGCGGGGAACACCCGGAGAGACTGACAGGGGACATCC 600
 Db 541 GTCCCTGACAGCAATGCTGTGCGGGGAACACCCGGAGAGACTGACAGGGGACATCC 600
 QY 601 GGAGGGCCCTGTGTGCAAGTGAATGGACACTGGCTGCAAGGGGGGGTGGTCACTGG 660
 Db 601 GGAGGGCCCTGTGTGCAAGTGAATGGACACTGGCTGCAAGGGGGGGTGGTCACTGG 660
 QY 661 GCGGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGCTGACTACTACTTGG 720
 Db 661 GCGGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGCTGACTACTACTTGG 720
 QY 721 GACTGGATTCACCACTATGTCCCAAAAAGCCGTGAACCGCCGCGCTGT 771
 Db 721 GACTGGATTCACCACTATGTCCCAAAAAGCCGTGAACCGCCGCGCTGT 771
 RESULT 11
 AAS20786
 ID AAS20786 standard; DNA; 771 BP.
 AC AAS20786;
 AC 09-APR-2002 (first entry)
 DR DNA encoding human beta-II trypsin active site mutant S194A #6.
 XX Human; proteolytic trypsin; protease; recombinant beta-II trypsin;
 KW enzyme; mutant; ds.
 KW
 KW Homo sapiens.
 OS Synthetic.
 OS MO200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US19681.
 XX 21-JUN-2000; 2000US-0598982.
 PA (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 DR WPI: 2002-114578/15.
 DR P-PSDB: AAU12020.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic
 PT trypsin, comprises DNA sequence encoding proteolytic trypsin having
 PT an active site mutation -
 XX
 XX Claim 7; Page 113-114; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic
 CC trypsin, active site mutants of these trypsin and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a

proteolytic trypsinase with an active site mutation (the construct drives expression of a mature proteolytic trypsinase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II trypsinase. The active site mutants of proteolytic trypsinase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic trypsinase produced are used as an antigen to generate anti-human trypsinase antibodies and in drug screening for compounds which act as trypsinase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II trypsinase active site mutants.

Sequence 771 BP; 152 A; 256 C; 240 G; 123 T; 0 other;

Query Match 97.7%; Score 753.4; DB 24; Length 771;
 Best Local Similarity 98.6%; Pred. No. 9.6e-145;
 Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1 GGGCCCTCGAGAAAAGATTCGTCGGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGG 60
 1 GGGCCCTCGAGAAAAGATTCGTCGGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGG 60
 61 CAGGTGAGCCTGAGAGTCCAGCGCCCAATGATGATGATGATGATGATGATGATGATGAT 120
 61 CAGGTGAGCCTGAGAGTCCAGCGCCCAATGATGATGATGATGATGATGATGATGATGAT 120
 61 CAGGTGAGCCTGAGAGTCCAGCGCCCAATGATGATGATGATGATGATGATGATGATGAT 120
 121 CAGCCCGAGTGGGTCTGACCGCGCGGGGTGCGGGGAGCCGAGGATGCAAGGATGCGGCC 180
 121 CAGCCCGAGTGGGTCTGACCGCGCGGGGTGCGGGGAGCCGAGGATGCAAGGATGCGGCC 180
 181 GCCCTCAGAGGCTCACTGGGGAGGAGCAGCCTTACTACGAGACAGAGTGGTGGCGGGT 240
 181 GCCCTCAGAGGCTCACTGGGGAGGAGCAGCCTTACTACGAGACAGAGTGGTGGCGGGT 240
 241 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 241 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 301 CTGGAGCTGAGGAGGAGCCGGTGAACGCTTCCAGCCAGCTTCCAGCCAGCTTCCAGCC 360
 301 CTGGAGCTGAGGAGGAGCCGGTGAACGCTTCCAGCCAGCTTCCAGCCAGCTTCCAGCC 360
 361 GCCTCAGAGGCTCACTGGGGAGGAGCAGCCTTACTACGAGACAGAGTGGTGGCGGGT 420
 361 GCCTCAGAGGCTCACTGGGGAGGAGCAGCCTTACTACGAGACAGAGTGGTGGCGGGT 420
 421 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 421 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 481 AACCAATTTTGTGAGCAGCAAAATATACCACTTGGCGCTTACAGGGAGACAGACCTCC 540
 481 AACCAATTTTGTGAGCAGCAAAATATACCACTTGGCGCTTACAGGGAGACAGACCTCC 540
 541 GTCCGTGAGCAGCAGTCTGTGTGCGGGGAAACACCCGAGGAGCACTATGCCAGCAGCT 600
 541 GTCCGTGAGCAGCAGTCTGTGTGCGGGGAAACACCCGAGGAGCACTATGCCAGCAGCT 600
 601 GAGGAGCCCTGTGTGTGCAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 660
 601 GAGGAGCCCTGTGTGTGCAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 660
 661 GCGGAGGAGGAGTGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 720
 661 GCGGAGGAGGAGTGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 720
 721 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
 721 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771

RESULT 12

AAS20779
 ID AAS20779 standard; DNA; 735 BP.
 NC AAS20779;
 DT 09-APR-2002 (first entry)
 DE DNA encoding human beta-II trypsinase active site mutant H44A #2.
 KW Human; proteolytic trypsinase; protease; recombinant beta-II trypsinase;
 KN enzyme; mutant; ds.
 OS Homo sapiens.
 OS Synthetic.
 PN W0200198470-A2.
 PD 27-DEC-2001.
 XX 20-JUN-2001; 2001W0-US19681.
 XX 21-JUN-2000; 2000US-0598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 DR WPI: 2002-114578/15.
 DR P-PSDB; AMU12013.
 PR DNA construct for producing enzymatically-inactive proteolytic
 PR trypsinase, comprises DNA sequence encoding proteolytic trypsinase having
 PR an active site mutation -
 XX
 XX
 PS Example 1c; Page 94-95; 126pp; English.
 CC The present invention relates to recombinant human proteolytic
 CC trypsinases, active site mutants of these trypsinases and the methods for
 CC producing these. The method involves the production of a DNA expression
 CC construct comprising a promoter operably linked to a secretion signal
 CC sequence which is operably linked to a DNA sequence encoding a
 CC proteolytic trypsinase with an active site mutation (the construct drives
 CC expression of a mature proteolytic trypsinase that lacks enzymatic activity
 CC due to the active site mutation, in hosts transformed to contain the
 CC construct). The method is useful for producing enzymatically-active
 CC beta-II trypsinase. The active site mutants of proteolytic trypsinase provide
 CC a tool to investigate the structural and functional properties of the
 CC protease and its enzymatic activity, and for modelling studies. The
 CC enzymatically-active, recombinant proteolytic trypsinase produced are
 CC useful as an antigen to generate anti-human trypsinase antibodies
 CC and in drug screening for compounds which act as trypsinase inhibitors,
 CC antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 CC human beta-II trypsinase active site mutants.
 CC
 XX
 SO Sequence 735 BP; 139 A; 245 C; 231 G; 120 T; 0 other;

Query Match 95.3%; Score 735; DB 24; Length 735;
 Best Local Similarity 100.0%; Pred. No. 5.4e-141;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 ATCGTCGGGGGTTCAGGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGAGTGGAGAGTGC 78
 19 ATCGTCGGGGGTTCAGGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGAGTGGAGAGTGC 78
 1 ATCGTCGGGGGTTCAGGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGAGTGGAGAGTGC 60
 1 ATCGTCGGGGGTTCAGGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGAGTGGAGAGTGC 60
 79 CAGGCCCATACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 138
 79 CAGGCCCATACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 138
 61 CAGGCCCATACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 61 CAGGCCCATACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 139 ACCGGCGGGGGTGGCGGAGCCGAGGAGTCAAGGATGATGATGATGATGATGATGATGAT 198
 139 ACCGGCGGGGGTGGCGGAGCCGAGGAGTCAAGGATGATGATGATGATGATGATGATGAT 198
 121 ACCGGCGGGGGTGGCGGAGCCGAGGAGTCAAGGATGATGATGATGATGATGATGATGAT 180
 121 ACCGGCGGGGGTGGCGGAGCCGAGGAGTCAAGGATGATGATGATGATGATGATGATGAT 180
 199 CGGGAGCAGCAGCTTACTACAGGAGCAGCAGTGTGCGCGGTACAGGAGATGATGATGATGAT 258

Db | 181 | GGGGAGCGACCTCTACTACCCAGGACCGAGCTGCCGGTACAGAGATCATCGTGCAC | 240
 Oy | 259 | CCACAGCTCTACACCGCCAGATGAGGAGGATCCGCTCCCTGGAGCTGAGAGAGCCG | 318
 Db | 241 | CCACAGCTCTACACCGCCAGATGAGGAGGATCCGCTCCCTGGAGCTGAGAGAGCCG | 300
 Oy | 319 | GTGAAGGTCTCCAGCCAGCTCCACCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG | 378
 Db | 301 | GTGAAGGTCTCCAGCCAGCTCCACCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG | 360
 Oy | 379 | CCGGGGATGCGGTGCTGGTCACTGGCTGGGGGCGATGTGGACAAATGATGAGCCCTCC | 438
 Db | 361 | CCGGGGATGCGGTGCTGGTCACTGGCTGGGGGCGATGTGGACAAATGATGAGCCCTCC | 420
 Oy | 439 | CCGGCAATTCCTGTAGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG | 498
 Db | 421 | CCGGCAATTCCTGTAGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG | 480
 Oy | 499 | AAATACCACTTGGGCGCTTACACGGGAGAGACGATCCGATCGCTCCGATGACGATGCTG | 558
 Db | 481 | AAATACCACTTGGGCGCTTACACGGGAGAGACGATCCGATCGCTCCGATGACGATGCTG | 540
 Oy | 559 | TGTGCGGGGAAACCCCGGAGGAGGATGATGATGATGATGATGATGATGATGATGATG | 618
 Db | 541 | TGTGCGGGGAAACCCCGGAGGAGGATGATGATGATGATGATGATGATGATGATGATG | 600
 Oy | 619 | AAGTGAATGGACCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 678
 Db | 601 | AAGTGAATGGACCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 660
 Oy | 679 | CCCAACCGGCTGGGATCTACACCGCTGTCACCTACTACTGAGTGGATGATCCACCACTAT | 738
 Db | 661 | CCCAACCGGCTGGGATCTACACCGCTGTCACCTACTACTGAGTGGATGATCCACCACTAT | 720
 Oy | 739 | GTCCCAAAAAAGCCG 735
 Db | 721 | GTCCCAAAAAAGCCG 735

Pr | an active site mutation -
 Xx |
 Ps | Example 1c: Page 115-117; 126pp; English.
 Cc | The present invention relates to recombinant human proteolytic
 Cc | trypsinases, active site mutants of these trypsinases and the methods for
 Cc | producing these. The method involves the production of a DNA expression
 Cc | construct comprising a promoter operably linked to a secretion signal
 Cc | sequence which is operably linked to a DNA sequence encoding a
 Cc | proteolytic trypsin with an active site mutation (the construct drives
 Cc | expression of a mature proteolytic trypsin that lacks enzymatic activity
 Cc | due to the active site mutation, in hosts transformed to contain the
 Cc | construct). The method is useful for producing enzymatically active
 Cc | beta-II trypsin. The active site mutants of proteolytic trypsin provide
 Cc | a tool to investigate the structural and functional properties of the
 Cc | protease and its enzymatic activity, and for modelling studies. The
 Cc | enzymatically active, recombinant proteolytic trypsin produced are
 Cc | useful as an antigen to generate anti-human trypsin antibodies
 Cc | and in drug screening for compounds which act as trypsin inhibitors,
 Cc | antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
 Cc | human beta-II trypsin active site mutants.
 S0 | Sequence 735 BP; 139 A; 246 C; 230 G; 120 T; 0 other:
 Query Match 95.1%; Score 733.4; DB 24; Length 735:
 Best Local Similarity 99.9%; Pred. No. 1,1e-140:
 Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
 Oy | 19 | ATGTCGGGGGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 78
 Db | 1 | ATGTCGGGGGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 60
 Oy | 79 | CACGGCCCACTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 138
 Db | 61 | CACGGCCCACTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 120
 Oy | 139 | ACCGGCCCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 198
 Db | 121 | ACCGGCCCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 180
 Oy | 199 | CCGGAGACAGACCTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT | 258
 Db | 181 | CCGGAGACAGACCTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT | 240
 Oy | 259 | CCACAGTCTTACACCGCCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 318
 Db | 241 | CCACAGTCTTACACCGCCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 300
 Oy | 319 | GTGAAGGTCTCCAGCCAGCTCCACCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG | 378
 Db | 301 | GTGAAGGTCTCCAGCCAGCTCCACCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG | 360
 Oy | 379 | CCGGGGATGCGGTGCTGGTCACTGGCTGGGGGCGATGTGGACAAATGATGAGCCCTCC | 438
 Db | 361 | CCGGGGATGCGGTGCTGGTCACTGGCTGGGGGCGATGTGGACAAATGATGAGCCCTCC | 420
 Oy | 439 | CCGGCAATTCCTGTAGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG | 498
 Db | 421 | CCGGCAATTCCTGTAGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG | 480
 Oy | 499 | AAATACCACTTGGGCGCTTACACGGGAGAGACGATCCGATCGCTCCGATGACGATGCTG | 558
 Db | 481 | AAATACCACTTGGGCGCTTACACGGGAGAGACGATCCGATCGCTCCGATGACGATGCTG | 540
 Oy | 559 | TGTGCGGGGAAACCCCGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG | 618
 Db | 541 | TGTGCGGGGAAACCCCGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG | 600
 Oy | 619 | AAGTGAATGGACCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 678
 Db | 601 | AAGTGAATGGACCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG | 660
 Oy | 679 | CCCAACCGGCTGGGATCTACACCGCTGTCACCTACTACTGAGTGGATGATCCACCACTAT | 738

DB 661 CCCAACCCGGCTGGCATCTAGACACCCTGTCACTACTACTGAGCATGCCACCTAT 720
 OY 739 GTCCCAAAAAGCCG 753
 DB 721 GTCCCAAAAAGCCG 735

RESULT 14
 AAV44330
 ID AAV44330 standard; DNA; 1128 BP.
 AC AAV44330;
 XX 24-NOV-1998 (first entry)

DE Human mast cell tryptase II/beta nucleic acid sequence.
 KW Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7;
 KW blood clot; anticoagulant; myocardial infarction; reocclusion;
 KW thromboembolism; cerebral embolism; thrombosis; therapy; ss.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 2..826
 FT CDS /*tag= a

PN MO9824886-A1.
 XX 11-JUN-1998.
 PD 25-NOV-1997; 97WO-US21620.
 PF 04-DEC-1996; 96US-0032354.
 PR (BGHM) BRIGHAM & WOMENS HOSPITAL.

PI Stevens RL;
 XX MPI: 1998-333308/29.
 DR P-PSDB; AAM64240.

PR New compositions containing tryptase-7, e.g. mouse mast cell
 protease-7 - are used to treat clot formation in e.g. myocardial
 infarction, reocclusion following angioplasty or pulmonary
 thromboembolism

PS Disclosure; Page 66; 92pp; English.

XX This nucleotide sequence includes a coding region for human
 CC mast cell tryptase II/beta (see AAM64240). The invention provides:
 CC compositions comprising an isolated tryptase-7 that may include
 CC chimeric proteins that contain (a) a human tryptase for all but
 CC the active site region and (b) the substrate-binding pocket of
 CC mouse tryptase-7 or its homologues (see AAM64233-39); a method for
 CC treating a blood clot by administering a nucleic acid molecule that
 CC codes for a tryptase-7, or an expression product, to decrease
 CC fibrinogen activity; a nucleic acid encoding a serine protease
 CC (SP); and a method of producing a mature SP by expressing the
 CC inactive zymogen in a host cell, and cleaving the enterokinase
 CC susceptibility domain. The tryptase-7 polypeptides can be used to
 CC treat disorders mediated by undesirable thrombus clot formation
 CC such as myocardial infarction and reocclusion following angioplasty
 CC of blood clots associated with pulmonary thromboembolism, deep vein
 CC thrombosis, cerebral embolism, renal vein and peripheral arterial
 CC thrombosis. They are also useful for all surgical procedures that
 CC require decreased blood clots.

XX Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 other;

Query Match 94.8%; Score 731; DB 19; Length 1128;
 Best Local Similarity 98.7%; Pred. No. 3.6e-140.

	Matches 737;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
OY 17	GAATGTCGGGGTTCAGGAGGCCCCCAGAGAGCAGTGGCCCTGGCAGGTGAGCCTGAGAG				76
DB 87	GCATCGTTGGGGGTAGGAGGGCCCCCAGAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG				146
OY 77	TCACGGCCATFATGATGCACTTCTGCGGGGGCTCCCTCATGCCACCAGTGGTGC				136
DB 147	TCACGGCCATFATGATGCACTTCTGCGGGGGCTCCCTCATGCCACCAGTGGTGC				206
OY 137	TGACCCGGCCGGCGTGGGGAGCCGACGTCAGAGATCGGGCCCTCAGGGGTCAAC				196
DB 207	TGACCCGGCCGGCGTGGGGAGCCGACGTCAGAGATCGGGCCCTCAGGGGTCAAC				266
OY 197	TGCGGAGCAGCAGCCTTACTACTACAGCAGCAGCTGCTCCGGTCCAGCAGATCATCTGC				256
DB 267	TGCGGAGCAGCAGCCTTACTACTACAGCAGCAGCTGCTCCGGTCCAGCAGATCATCTGC				326
OY 257	ACCACAGTCTACACCGCCAGATCGAGCGGAGACATGCCCTGTGGAGCTGAGAGAC				316
DB 327	ACCACAGTCTACACCGCCAGATCGAGCGGAGACATGCCCTGTGGAGCTGAGAGAC				386
OY 317	CGGTGAAGTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC				376
DB 387	CGGTGAAGTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC				446
OY 377	CCCCGGGAGTGGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				436
DB 447	CCCCGGGAGTGGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				506
OY 437	CACGGCCATTTTCCTGTGAAAGCAGTGAAGTCCCATTAATGAAACACATTTTGTGAC				496
DB 507	CACGGCCATTTTCCTGTGAAAGCAGTGAAGTCCCATTAATGAAACACATTTTGTGAC				566
OY 497	CAAAATPACACCTTGGCGCTACCGGGAGCAGCAGTCCGATGCTCCGTTGACGACATGC				556
DB 567	CAAAATPACACCTTGGCGCTACCGGGAGCAGCAGTCCGATGCTCCGTTGACGACATGC				626
OY 557	TGTGTGGCGGGAACACCCGGAGGACTATGCCAGGCGCTCCGGAGGGCCCTGTGGT				616
DB 627	TGTGTGGCGGGAACACCCGGAGGACTATGCCAGGCGCTCCGGAGGGCCCTGTGGT				686
OY 617	GCAAGGTGATGGACCTGCTGCAAGCGGGCGTGTCACTGGGGCCAGGGCTGTGCC				676
DB 687	GCAAGGTGATGGACCTGCTGCAAGCGGGCGTGTCACTGGGGCCAGGGCTGTGCC				746
OY 677	AGCCCAACCCGGCTGGCATCTACACCCGTTGACCTTGGACATGGATCCACCACT				736
DB 747	AGCCCAACCCGGCTGGCATCTACACCCGTTGACCTTGGACATGGATCCACCACT				806
OY 737	ATGTCCCCAAAAGCCGTGMAAGCGGCC				763
DB 807	ATGTCCCCAAAAGCCGTGMAAGCGGCC				833
RESULT 15					
AAV42712	ID AAV42712 standard; cDNA; 1128 BP.				
XX AAV42712;					
XX 27-OCT-1998 (first entry)					
DE Human mast cell tryptase II/beta encoding cDNA.					
XX Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;					
XX KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;					
XX KW angioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;					
XX KW hyperproliferative skin disease; peptic ulcer; hypersensitivity;					
XX KW inflammatory skin condition; human; mast cell tryptase II/beta; ss.					
XX Homo sapiens.					

```

FH Key Location/Qualifiers
FT CDS 2..826
FT /*tag= a
FT /product= "Human mast cell tryptase II/beta"
FT /note= "the start codon is not indicated"
XX
XX WO9833812-A1.
XX
XX
XX 06-AUG-1998.
XX
XX
XX 30-JAN-1998; 98MO-USO1865.
XX
XX 05-FEB-1997; 97US-0037090.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Huang C, Stevens RL;
XX
XX WPI: 1998-437390/37.
XX
XX P-PSDB: AAM63175.
XX
XX
XX Tryptase-6 complex inhibitory peptides - used to treat mast
XX cell-mediated inflammatory disorders e.g. asthma
XX
XX PS Disclosure; Pages 47-48; 69pp; English.
XX
XX
XX This cDNA encodes the human mast cell tryptase II/beta which is a
XX homologue of the mouse mast cell protease (mMCP-6) zymogen. The
XX invention provides sequences shown in AAM63160 to AAM63169 that are
XX inhibitors of mMCP-6. These peptides which are tryptase-6 complex
XX inhibitors, can be used for treating a mast cell-mediated inflammatory
XX disorder. The inhibitors can be used to treat inflammatory disorders
XX including asthma, allergic rhinitis, urticaria and angioedema,
XX eczematous dermatitis (atopic dermatitis), anaphylaxis,
XX hyperproliferative skin disease, peptic ulcers, inflammatory bowel
XX disorder, hypersensitivity and inflammatory skin conditions.
XX
XX SQ Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 other:
  
```

```

Query Match 94.8%; Score 731; DB 19; Length 1128;
Best Local Similarity 98.7%; Pred. No. 3.6e-140;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
  
```

```

OY 17 GAATGTCGGGGGTCAGAGGCCCCCAGAGCAGATGGCCCTGGCAGGTGAGCCTGAGAG 76
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 87 GCATTCGTTGGGGGTCAGAGGCCCCCAGAGCAGATGGCCCTGGCAGGTGAGCCTGAGAG 146
OY 77 TCACAGGCGCATACTGATGACGTTGCGGGGGGCTCCCTCATCCACCCAGTGGGTGC 136
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 147 TCCAGGCGCATACTGATGACGTTGCGGGGGGCTCCCTCATCCACCCAGTGGGTGC 206
OY 137 TGACCAGCGGGCGGTGGCGTGACCGGCATGCAAGATCTGGCCCGCCCTCAGGGTGAAC 196
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 207 TGACCGCAGCGACTGTGGACCAGGACGTCAGAGATCTGGCCCGCCCTCAGGGTGAAC 266
OY 197 TGGGGAACAGCACCCTACTAACCAGCAGCTGCTGCGGTGAGCAAGCATCGTGC 256
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 267 TGGGGAGACAGCACCCTACTAACCAGCAGCTGCTGCGGTGAGCAAGCATCGTGC 326
OY 257 ACCGACAGTTCATCACCAGCTCCACAGGAGGAGCATCGCCCTGAGGCTGGAGAGC 316
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 ACCGACAGTTCATCACCAGCTCCACAGGAGGAGCATCGCCCTGAGGCTGGAGAGC 386
OY 317 CGGTAAAGTTCATCACCAGCTCCACAGGAGGAGCATCGCCCTGAGGCTGGAGAGC 376
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 387 CGGTAAAGTTCATCACCAGCTCCACAGGAGGAGCATCGCCCTGAGGCTGGAGAGC 446
OY 377 CCCCCGGGATGCCGTGCTGAGGCTCATGCGCTGAGGAGGATGGACAAATGATGAGCCCTCC 436
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 447 CCCCCGGGATGCCGTGCTGAGGCTCATGCGCTGAGGAGGATGGACAAATGATGAGCCCTCC 506
OY 437 CACCGCATTTTCTGTAAGCAGTGAAGGTCCCATTAATGAAAAACACATTTTGTAAGC 496
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  
```

```

Db 507 CACCGCATTTTCTGTAAGCAGTGAAGGTCCCATTAATGAAAAACACATTTTGTAAGC 566
OY 497 CAAATFACCACCTTGCGGGCTTACACAGGAGGAGCAGCATCGCTCCGATGCTCCGTAGCACATGC 556
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 567 CAAATFACCACCTTGCGGGCTTACACAGGAGGAGCAGCATCGCTCCGATGCTCCGTAGCACATGC 626
OY 557 TGTGTGCCGGGAAACACCCCGGAGGACTCATGTCCAGAGGGCCCTCTGTGTGT 616
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 627 TGTGTGCCGGGAAACACCCCGGAGGACTCATGTCCAGAGGGCCCTCTGTGTGT 686
OY 617 GCAAAGTGAATGGACCTGCTGCAAGCGGCGGTGTGATCAGTGGGGCGAGGGCTGTGTGCC 676
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 687 GCAAAGTGAATGGACCTGCTGCAAGCGGCGGTGTGATCAGTGGGGCGAGGGCTGTGTGCC 746
OY 677 AGCCCAACCGGCTGGCATTTCACACCCGCTGCACCTACTTGGACTGTGATCCACCCT 736
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 747 AGCCCAACCGGCTGGCATTTCACACCCGCTGCACCTACTTGGACTGTGATCCACCCT 806
OY 737 ATGTCCCAAAAAAGCGTGAAGCGGCC 763
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 807 ATGTCCCAAAAAAGCGTGAAGCGGCC 833
  
```

Search completed: January 31, 2003, 05:24:05
Job time : 274 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 04:47:55 ; Search time 2796 Seconds
(without alignments) 8025.130 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 771
Sequence: 1 gggcccccctcagagaagaat.....cgtcgaagcgccgcgtcgt 771

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: GenBml:*
- 2: gb_da:*
- 3: gb_htg:*
- 4: gb_la:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_mu:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rtd:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771	100.0	771	6 AX347853	AX347853 Sequence
2	769.4	99.8	771	6 AX347869	AX347869 Sequence
3	764.6	99.2	771	6 ARI65112	ARI65112 Sequence
4	764.6	99.2	771	6 AX347841	AX347841 Sequence
5	763	99.0	771	6 AX347838	AX347838 Sequence
6	761.4	98.8	771	6 AX347855	AX347855 Sequence
7	759.8	98.5	771	6 AX347871	AX347871 Sequence
8	755	97.9	771	6 AX347857	AX347857 Sequence
9	755	97.9	771	6 AX347859	AX347859 Sequence
10	753.4	97.7	771	6 AX347873	AX347873 Sequence
11	753.4	97.7	771	6 AX347875	AX347875 Sequence
12	735	95.3	735	6 AX347861	AX347861 Sequence
13	733.4	95.1	735	6 AX347877	AX347877 Sequence
14	731	94.8	1128	6 AR080461	AR080461 Sequence
15	731	94.8	1128	6 HUMTRX2A	HUMTRX2A Sequence
16	731	94.8	1137	6 AR080460	AR080460 Sequence
17	731	94.8	1137	9 HUMTRX1A	HUMTRX1A Sequence
18	731	94.8	1143	9 HUMBRTRYP	HUMBRTRYP Sequence
19	731	94.8	1145	9 S5551	S5551 beta-trypt
20	731	94.8	1194	9 BC029356	BC029356 Homo sapi
21	728.6	94.5	735	6 ARI65109	ARI65109 Sequence
22	728.6	94.5	735	6 AX347843	AX347843 Sequence
23	727	94.3	735	6 AX347834	AX347834 Sequence
24	726.2	94.2	1081	6 AR080462	AR080462 Sequence
25	726.2	94.2	1081	6 AX329646	AX329646 Sequence
26	726.2	94.2	1081	6 AX330205	AX330205 Sequence
27	726.2	94.2	1081	6 AX334644	AX334644 Sequence
28	726.2	94.2	1081	6 AX375047	AX375047 Sequence
29	726.2	94.2	1081	9 HUMTRX3A	HUMTRX3A Sequence
30	725.4	94.1	735	6 AX347863	AX347863 Sequence
31	723.8	93.9	735	6 AX347879	AX347879 Sequence
32	719	93.3	735	6 AX347865	AX347865 Sequence
33	719	93.3	735	6 AX347867	AX347867 Sequence
34	719	93.3	1221	6 AX014344	AX014344 Sequence
35	718.2	93.2	2662	6 AX338508	AX338508 Sequence
36	717.4	93.0	735	6 AX347881	AX347881 Sequence
37	717.4	93.0	735	6 AX347883	AX347883 Sequence
38	692.6	89.8	884	9 AF206665	AF206665 Homo sapi
39	692.6	89.8	1206	9 BC028059	BC028059 Homo sapi
40	686.2	89.0	1154	6 AR080459	AR080459 Sequence
41	686.2	89.0	1154	9 HUMTRX	M30038 Human trypt
42	630.2	81.7	768	9 AF206666	AF206666 Homo sapi
43	597.6	77.5	918	9 AF206667	AF206667 Homo sapi
44	539.4	70.0	661	9 AF206664	AF206664 Homo sapi
45	519.6	67.4	995	4 DOGMCTRPA	M24664 Dog mast ce

ALIGNMENTS

RESULT 1
AX347853
LOCUS AX347853 771 bp DNA
DEFINITION Sequence 20 from Patent WO0198470.
ACCESSION AX347853
VERSION AX347853.1 GI:18495660
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Maffei, M., Niles, A.L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same

JOURNAL Patent: WO 0198470-A 20 27-DEC-2001;
 PROMEGA CORPORATION (US)
 Location/Qualifiers
 source 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <1..756
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22420.1"
 /_id_xref="GI:18495677"
 /translation="LEKRRIVGGQEPARPSKMPQVSLRVHGPYWMHFEKGGSLIHPQV
 VLRPAACVGPDKDLALRVQLREOHLYQDQLPVRILVHPQEPYTAQIGADLALLE
 LEPVVSSHVHTVTLRPAASETEPPGMPQWVTDNDELRPLPPEPLKQVPIEMN
 NHICDAKYHLGAVTGDVRIYRDMMLCAGNTRRSDSQDGGPRLVCKVNGWTLQAGVY
 SMEBGCQPNRPGIYTRVYIYLDIMHHVYKPKP"

BASE COUNT 147 a 256 c 244 g 124 t
 ORIGIN
 Query Match 100.0%; Score 771; DB 6; Length 771;
 Best Local Similarity 100.0%; Pred. No. 1,4e-117;
 Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAGAAAAAAGATGCTGGGGTCAAGAGGCCCCCAGGAGCAAGTGGCCCTG 60
 |||
 DB 1 GGGCCCTCGAGAAAAAAGATGCTGGGGTCAAGAGGCCCCCAGGAGCAAGTGGCCCTG 60
 QY 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 |||
 DB 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 QY 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 |||
 DB 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 QY 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 |||
 DB 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 QY 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 |||
 DB 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 QY 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 |||
 DB 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 QY 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 |||
 DB 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 QY 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 |||
 DB 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 QY 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 |||
 DB 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 QY 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 |||
 DB 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 QY 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 |||
 DB 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 QY 361 GCTTCAGAGACCTTCCCGCGGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 |||
 DB 361 GCTTCAGAGACCTTCCCGCGGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 421 AATGATGAGCGCCCTCCACCGCATTTCTGTAAGGAGGAGTCCCATTAATGGAA 480
 |||
 DB 421 AATGATGAGCGCCCTCCACCGCATTTCTGTAAGGAGGAGTCCCATTAATGGAA 480
 QY 421 AATGATGAGCGCCCTCCACCGCATTTCTGTAAGGAGGAGTCCCATTAATGGAA 480
 |||
 DB 421 AATGATGAGCGCCCTCCACCGCATTTCTGTAAGGAGGAGTCCCATTAATGGAA 480
 QY 481 AACCAATTTGTGAGAGCAAAATACCACTTGGCGCTCACGGAGAGACGTCGCCCATC 540
 |||
 DB 481 AACCAATTTGTGAGAGCAAAATACCACTTGGCGCTCACGGAGAGACGTCGCCCATC 540
 QY 481 AACCAATTTGTGAGAGCAAAATACCACTTGGCGCTCACGGAGAGACGTCGCCCATC 540
 |||
 DB 481 AACCAATTTGTGAGAGCAAAATACCACTTGGCGCTCACGGAGAGACGTCGCCCATC 540
 QY 541 GTCGCTGACGACATGCTGTGTGCGCGGGAACCCGGAAGGACCTCATGCGCAGGCGATCC 600
 |||
 DB 541 GTCGCTGACGACATGCTGTGTGCGCGGGAACCCGGAAGGACCTCATGCGCAGGCGATCC 600
 QY 601 GGAGGGCCCTGTGTGTAAGGTGAATGGACCTGTGGCGAGGGGGGGTGTGCTGAGCTGG 660
 |||
 DB 601 GGAGGGCCCTGTGTGTAAGGTGAATGGACCTGTGGCGAGGGGGGGTGTGCTGAGCTGG 660
 QY 601 GGAGGGCCCTGTGTGTAAGGTGAATGGACCTGTGGCGAGGGGGGGTGTGCTGAGCTGG 660
 |||
 DB 601 GGAGGGCCCTGTGTGTAAGGTGAATGGACCTGTGGCGAGGGGGGGTGTGCTGAGCTGG 660
 QY 661 GGCGAGGGCTGTGCGCCAGCCCAACCGCGCTGGCATCTACCCCGTGTACTACTTGG 720
 |||
 DB 661 GGCGAGGGCTGTGCGCCAGCCCAACCGCGCTGGCATCTACCCCGTGTACTACTTGG 720
 QY 721 GACTGGATCCACCACTATGTCCCAAAAAAGCGGTGAAGCGGGCCGCTGCT 771
 |||
 DB 721 GACTGGATCCACCACTATGTCCCAAAAAAGCGGTGAAGCGGGCCGCTGCT 771

DB 721 GACTGGATCCACCACTATGTCCCAAAAAAGCGGTGAAGCGGGCCGCTGCT 771

RESULT 2
 AX347869
 LOCUS AX347869 771 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 36 from Patent WO0198470.
 ACCESSION AX347869
 VERSION AX347869.1 GI:18495676
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
 1 Maffei, M., Niles, A.L. and Haak-Frendscho, M.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 JOURNAL Patent: WO 0198470-A 36 27-DEC-2001;
 PROMEGA CORPORATION (US)
 Location/Qualifiers
 source 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7..756
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22428.1"
 /_id_xref="GI:18495677"
 /translation="LEKRRIVGGQEPARPSKMPQVSLRVHGPYWMHFEKGGSLIHPQV
 VLRPAACVGPDKDLALRVQLREOHLYQDQLPVRILVHPQEPYTAQIGADLALLE
 LEPVVSSHVHTVTLRPAASETEPPGMPQWVTDNDELRPLPPEPLKQVPIEMN
 ICDARKYHLGAVTGDVRIYRDMMLCAGNTRRSDSQDGGPRLVCKVNGWTLQAGVY
 SMEBGCQPNRPGIYTRVYIYLDIMHHVYKPKP"

BASE COUNT 147 a 257 c 243 g 124 t
 ORIGIN
 Query Match 99.8%; Score 769.4; DB 6; Length 771;
 Best Local Similarity 99.9%; Pred. No. 2.5e-117;
 Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAGAAAAAAGATGCTGGGGTCAAGAGGCCCCCAGGAGCAAGTGGCCCTG 60
 |||
 DB 1 GGGCCCTCGAGAAAAAAGATGCTGGGGTCAAGAGGCCCCCAGGAGCAAGTGGCCCTG 60
 QY 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 |||
 DB 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 QY 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 |||
 DB 61 CAGTGAACCTCGAAGTCCAGGCGCATACAGTACGATGACATCTGCGGGGCTCCCTCATC 120
 QY 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 |||
 DB 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 QY 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 |||
 DB 121 CACCCCAAGTGGTGTACCCGCGCGCGTGTGGGAGCCGAGAGTCAAGATGTGGCC 180
 QY 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 |||
 DB 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 QY 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 |||
 DB 181 GCCCTCAAGGTTGCAACCTGCGGAGAGCACTTAACAGAGACCAGCTGCTGGCGGT 240
 QY 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 |||
 DB 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 QY 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 |||
 DB 241 AGCAGGATCATATGTCACCCACCAAGTTCACACCGCCCAAGTCGGAGACATGGCCCTG 300
 QY 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 |||
 DB 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 QY 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 |||
 DB 301 CTGAGCTGTGAGAGCCGCGTGAAGTCTCCAGCCAGTCCACACCGTGCACCTGGCCCCCT 360
 QY 361 GCTTCAGAGACCTTCCCGCGGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 |||
 DB 361 GCTTCAGAGACCTTCCCGCGGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 421 AATGATGAGCGCCCTCCACCGCATTTCTGTAAGGAGGAGTCCCATTAATGGAA 480
 |||
 DB 421 AATGATGAGCGCCCTCCACCGCATTTCTGTAAGGAGGAGTCCCATTAATGGAA 480

QY 481 AACCAATTTGTGACGCAAAATACCACTTGGCCGCTACACGGAGAGACAGCTCCGCATC 540
 Db 481 AACCAATTTGTGACGCAAAATACCACTTGGCCGCTACACGGAGAGAGAGCTCCGCATC 540
 QY 541 GTCGCTGACGACATGCTGTGTGCGGGAAACACCCGGAGGACTCATGCCAGGGCCATCC 600
 Db 541 GTCGCTGACGACATGCTGTGTGCGGGAAACACCCGGAGGACTCATGCCAGGGCCATCC 600
 QY 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGCTGCACAGGGGGGGTGGTCAAGCTGG 660
 Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGCTGCACAGGGGGGGTGGTCAAGCTGG 660
 QY 661 GGCGAGGGCTGTGTGCCAGCCCAACCGCCCTGGCATCTACACCCCTGTCTACCTACTG 720
 Db 661 GGCGAGGGCTGTGTGCCAGCCCAACCGCCCTGGCATCTACACCCCTGTCTACCTACTG 720
 QY 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGTGAAGCGGGCCGCTGCT 771
 Db 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGTGAAGCGGGCCGCTGCT 771

RESULT 3
 ARI65112
 LOCUS ARI65112 771 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 4 from patent US 6274366.
 ACCESSION ARI65112
 VERSION ARI65112.1 GI:16238527
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 771)
 AUTHORS Maffitt,M.A., Niles,A.L. and Haak-Frendscho,M.
 TITLE Enzymatically-active recombinant human .beta.-tryptase and method
 of making same
 JOURNAL Patent: US 6274366-A 4 14-AUG-2001;
 FEATURES
 source Location/Qualifiers
 1..771
 /organism="unknown"

BASE COUNT 149 a 256 c 242 g 124 t
 ORIGIN
 Query Match 99.2%; Score 764.6; DB 6; Length 771;
 Best Local Similarity 99.5%; Pred. No. 1.6e-116;
 Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGGCCCCCTCGAGAAAAGAAATGCTGGGGGTGAGGAGCCGCCAGAGCAAGTGGCCCTGG 60
 Db 1 GGGCCCCCTCGAGAAAAGAAATGCTGGGGGTGAGGAGCCGCCAGAGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCCTGAGAGATCCACGGCCCATATCTGATGCACTTCTGGGGGGCTCCCTCATC 120
 Db 61 CAGGTGAGCCTGAGAGATCCACGGCCCATATCTGATGCACTTCTGGGGGGCTCCCTCATC 120
 QY 121 CACCCCGAGTGGGTCTGACCCGCCGGCGCTGCGGAGCCGGAGCTCAAGGATCTGGCC 180
 Db 121 CACCCCGAGTGGGTCTGACCCGCCGGCGCTGCGGAGCCGGAGCTCAAGGATCTGGCC 180
 QY 181 GCCCTCAGGGGTCAACTGCGGGGAGAGCACTTACTACTACAGGACCAAGCTGCTGCCGGT 240
 Db 181 GCCCTCAGGGGTCAACTGCGGGGAGAGCACTTACTACTACAGGACCAAGCTGCTGCCGGT 240
 QY 241 AGCAGGATCATGCTCAGCCACAGTTTCTACACCGCCCAAGTGGAGCGGACATCGCCCTG 300
 Db 241 AGCAGGATCATGCTCAGCCACAGTTTCTACACCGCCCAAGTGGAGCGGACATCGCCCTG 300
 QY 301 CTGAGCTGAGAGACCGGTGAAGGCTTCCAGCCAGCTCCACAGCGGTCACTCCCTGCCCT 360
 Db 301 CTGAGCTGAGAGACCGGTGAAGGCTTCCAGCCAGCTCCACAGCGGTCACTCCCTGCCCT 360
 QY 361 GCCTCAGAGACTTCCCTCCCGGGGATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 361 GCCTCAGAGACTTCCCTCCCGGGGATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 AATGATGAGCGGCTTCCCAACCGCCATTTTCTGAAAGCAAGTGAAGTCCCTTAATGGA 480
 Db 421 AATGATGAGCGGCTTCCCAACCGCCATTTTCTGAAAGCAAGTGAAGTCCCTTAATGGA 480
 QY 481 AACCAATTTGTGACGCAAAATACCACTTGGCCGCTACACGGAGAGAGAGCTCCGCATC 540
 Db 481 AACCAATTTGTGACGCAAAATACCACTTGGCCGCTACACGGAGAGAGAGCTCCGCATC 540
 QY 541 GTCGCTGACGACATGCTGTGTGCGGGAAACACCCGGAGGACTCATGCCAGGGCCATCC 600
 Db 541 GTCGCTGACGACATGCTGTGTGCGGGAAACACCCGGAGGACTCATGCCAGGGCCATCC 600
 QY 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGCTGCACAGGGGGGGTGGTCAAGCTGG 660
 Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGCTGCACAGGGGGGGTGGTCAAGCTGG 660
 QY 661 GGCGAGGGCTGTGTGCCAGCCCAACCGCCCTGGCATCTACACCCCTGTCTACCTACTG 720
 Db 661 GGCGAGGGCTGTGTGCCAGCCCAACCGCCCTGGCATCTACACCCCTGTCTACCTACTG 720
 QY 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGTGAAGCGGGCCGCTGCT 771
 Db 721 GACTGGATCCACCACTATGTCTCCCAAAAAAGCCGTGAAGCGGGCCGCTGCT 771

RESULT 4
 AX347841
 LOCUS AX347841 771 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 8 from patent WO0198470.
 ACCESSION AX347841
 VERSION AX347841.1 GI:18495648
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Maffitt,M., Niles,A.L. and Haak-Frendscho,M.
 TITLE Recombinant proteolytic tryptases, active site mutants thereof, and
 methods of making same
 JOURNAL Patent: WO 0198470-A 8 27-DEC-2001;
 FEATURES
 source Location/Qualifiers
 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7..756
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="GAD22418.1"
 /db_xref="GI:18495648"
 /translation="LEKRTVGGQDAPRNSKWPQVSLRVHGFYWHHFCGGSLIHPOWLV
 /TAACVAGPDVYKDLAALRYQLREOHLYVQDOLPVSRIIVHPOFTTAQIGADIALLEIE
 EPRVYVSSHVHTVTLRPAEETPEPMPGCVTGMVDNDELRPPEPKQYVLPIMENH
 ICDDKYHNGAVTGDVRIYRDMDCAGTTRDSDQQGSGSGLYVKVNGTMIQAGVYSW
 GEGCAQPRPRITVRYRMYIYLDWIIHLYPKR*"

BASE COUNT 149 a 256 c 242 g 124 t
 ORIGIN
 Query Match 99.2%; Score 764.6; DB 6; Length 771;
 Best Local Similarity 99.5%; Pred. No. 1.6e-116;
 Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGGCCCCCTCGAGAAAAGAAATGCTGGGGGTGAGGAGCCGCCAGAGCAAGTGGCCCTGG 60
 Db 1 GGGCCCCCTCGAGAAAAGAAATGCTGGGGGTGAGGAGCCGCCAGAGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCCTGAGAGATCCACGGCCCATATCTGATGCACTTCTGGGGGGCTCCCTCATC 120
 Db 61 CAGGTGAGCCTGAGAGATCCACGGCCCATATCTGATGCACTTCTGGGGGGCTCCCTCATC 120
 QY 121 CACCCCGAGTGGGTCTGACCCGCCGGCGCTGCGGAGCCGGAGCTCAAGGATCTGGCC 180

```

|||||
Db 121 CACCCCAAGTGGTGTGACCCGACCCACCTGCGTGGAGCCGGACGTCMAAGATCTGGCC 180
|||
Qy 181 GCCCTCAGGGGGAACATGCGGGGAGCAGACCTCTACTACCAGACGATCTGCTCCGGTC 240
|||
Db 181 GCCCTCAGGGGGAACATGCGGGGAGCAGACCTCTACTACCAGACGATCTGCTCCGGTC 240
|||
Qy 241 AGCAGATCATCTGTGACACCACAGTCTTACACCCGCCAGATCGGAGCGGACATCGCCCTG 300
|||
Db 241 AGCAGATCATCTGTGACACCACAGTCTTACACCCGCCAGATCGGAGCGGACATCGCCCTG 300
|||
Qy 301 CTGGAGCTGGAAGAGCCGGTGAAGGTTCCAGCCATCCACAGGTCACCTCTCCCTCCCT 360
|||
Db 301 CTGGAGCTGGAAGAGCCGGTGAAGGTTCCAGCCATCCACAGGTCACCTCTCCCTCCCT 360
|||
Qy 361 GCCCTCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Db 361 GCCCTCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Qy 421 AATGATGAGCCCTCCACCCGCAATTTCTCTGAAGCAGGTGAAGGTCCTCCATTAATGAA 480
|||
Db 421 AATGATGAGCCCTCCACCCGCAATTTCTCTGAAGCAGGTGAAGGTCCTCCATTAATGAA 480
|||
Qy 481 AACCAATTTGTGACGCAAAAATACCACCTTGGCCCTTACAGGGAGACAGTCCGGCATC 540
|||
Db 481 AACCAATTTGTGACGCAAAAATACCACCTTGGCCCTTACAGGGAGACAGTCCGGCATC 540
|||
Qy 541 GTCCTGACGACATCTGTGTGTCGGGGAAACACCCGGAGGATCTGACAGGGGATGTGGAC 600
|||
Db 541 GTCCTGACGACATCTGTGTGTCGGGGAAACACCCGGAGGATCTGACAGGGGATGTGGAC 600
|||
Qy 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGTCGACAGGGGCGGTGTGACGTGG 660
|||
Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGTCGACAGGGGCGGTGTGACGTGG 660
|||
Qy 661 GCGCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Db 661 GCGCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Qy 721 GACTGGATCCACCACTATGTGCCCAAAAAGCGGTGAAGCGGGCCGCTGCTG 771
|||
Db 721 GACTGGATCCACCACTATGTGCCCAAAAAGCGGTGAAGCGGGCCGCTGCTG 771
|||
RESULT 5
AX347838 771 bp DNA linear PAT 01-FEB-2002
LOCUS AX347838
DEFINITION Sequence 5 from Patent W00198470.
ACCESSION AX347838
VERSION AX347838.1 GI:18495645
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Maffei,M., Niles,A.D. and Haak-Frendscho,M.
AUTHORS Recombinant proteolytic tryptases, active site mutants thereof, and
TITLE Methods of making same
JOURNAL Patent: WO 0198470-A 5 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
SOURCE Location/Qualifiers
1..771
/organism="Homo sapiens"
/db_xref="taxon:9606"
<7..756
/note="unnamed protein product"
CDS
/protein_id="CAD22417.1"
/db_xref="GI:18495646"
/translation="LEKRIVGGQEAAPRSKWPMOVSLRVHGPHYMHFGGSLIHPOWLV
TRANCGPDVYKDLALRYLREOHLYKODOLLYPSRITVHPOFTYAOIGADIALLELE
EPVNVSSHVHTVTLPPASEIFPPGHPGFWVDTGMDVDDNDERLDRPPPLKQVYVPIWENH

```

```

IDDAKYNLHAGTVDVYKDLRYLREOHLYKODOLLYPSRITVHPOFTYAOIGADIALLELE
GEGCQADPNRPGITTYRVTYLYDMTHNHPKPP"
BASE COUNT 149 a 257 c 241 g 124 t
ORIGIN
Query Match 99.0%; Score 763; DB 6; Length 771;
Best Local Similarity 99.4%; Pred. No. 2, 9e-116;
Matches 766; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GGGCCCTCGAAGAAAAGATTCGGGGGTCAGAGAGCCCGCCAGAGCAAGTGGCCCTGG 60
|||
Db 1 GGGCCCTCGAAGAAAAGATTCGGGGGTCAGAGAGCCCGCCAGAGCAAGTGGCCCTGG 60
|||
Qy 61 CAGGTGAGCCCTGAGAGATTCACAGGGCCCATCTGATGATGATGATGATGATGATGATG 120
|||
Db 61 CAGGTGAGCCCTGAGAGATTCACAGGGCCCATCTGATGATGATGATGATGATGATGATG 120
|||
Qy 121 CACCCCAAGTGGTGTGACCCCGCCGGGATGCGTGGGAGCCGAGCATTAAGATCTGGCC 180
|||
Db 121 CACCCCAAGTGGTGTGACCCCGCCGGGATGCGTGGGAGCCGAGCATTAAGATCTGGCC 180
|||
Qy 181 GCCCTCAGGGGTCACACTGGGGAGCAGACCTCTACTACCAGAGACAGTCTGCGGGTC 240
|||
Db 181 GCCCTCAGGGGTCACACTGGGGAGCAGACCTCTACTACCAGAGACAGTCTGCGGGTC 240
|||
Qy 241 AGCAGATCATCTGTGACACCACAGTCTTACACCCGCCAGATCGGAGCGGACATCGCCCTG 300
|||
Db 241 AGCAGATCATCTGTGACACCACAGTCTTACACCCGCCAGATCGGAGCGGACATCGCCCTG 300
|||
Qy 301 CTGGAGCTGGAAGAGCCGGTGAAGGTTCCAGCCATCCACAGGTCACCTCTCCCTCCCT 360
|||
Db 301 CTGGAGCTGGAAGAGCCGGTGAAGGTTCCAGCCATCCACAGGTCACCTCTCCCTCCCT 360
|||
Qy 361 GCGCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Db 361 GCGCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Qy 421 AATGATGAGCCCTCCACCCGCAATTTCTCTGAAGCAGGTGAAGGTCCTCCATTAATGAA 480
|||
Db 421 AATGATGAGCCCTCCACCCGCAATTTCTCTGAAGCAGGTGAAGGTCCTCCATTAATGAA 480
|||
Qy 481 AACCAATTTGTGACGCAAAAATACCACCTTGGCCCTTACAGGGAGACAGTCCGGCATC 540
|||
Db 481 AACCAATTTGTGACGCAAAAATACCACCTTGGCCCTTACAGGGAGACAGTCCGGCATC 540
|||
Qy 541 GTCCTGACGACATCTGTGTGTCGGGGAAACACCCGGAGGATCTGACAGGGGATGTGGAC 600
|||
Db 541 GTCCTGACGACATCTGTGTGTCGGGGAAACACCCGGAGGATCTGACAGGGGATGTGGAC 600
|||
Qy 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGTCGACAGGGGCGGTGTGACGTGG 660
|||
Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGTCGACAGGGGCGGTGTGACGTGG 660
|||
Qy 661 GCGCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Db 661 GCGCAGAGACCTTCCCGCCGGGATGCGTGGGTCACCTGGCTGGGGGATGTGGAC 420
|||
Qy 721 GACTGGATCCACCACTATGTGCCCAAAAAGCGGTGAAGCGGGCCGCTGCTG 771
|||
Db 721 GACTGGATCCACCACTATGTGCCCAAAAAGCGGTGAAGCGGGCCGCTGCTG 771
|||
RESULT 6
AX347855 771 bp DNA linear PAT 01-FEB-2002
LOCUS AX347855
DEFINITION Sequence 22 from Patent W00198470.
ACCESSION AX347855
VERSION AX347855.1 GI:18495662
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

REFERENCE 1
 AUTHORS Maffei, M., Niles, A.L. and Haak-Frendscho, M.
 TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and
 methods of making same
 JOURNAL Patent: WO 0198470-A 22 27-DEC-2001;
 PROMEGA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7..736
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22429.1"
 /db_xref="GI:18495678"
 /translation="LEKRIVGGQEARPKRPMQVSLRVHGRPMHFGGSLIHQWVW
 TAARVGFVDVLDLALRYQLREQHLXYDQDLPLVSRILVHPQFYTAQGAIALLELE
 EPVYVSSHVHTVLPAPSETRPPGMPGCVTGMGDVNDERLPPPEPLKQVYPIWENH
 ICDARVHGAYTGDDVRIYRDMDCAGNTRDSCQDGGGGLVCKVNGTWMLOAGVYVSW
 GEGCAQPRPPIYTRVRYLLDMIHNYVYKRP"

BASE COUNT 149 a 256 c 242 g 124 t
 ORIGIN
 Query Match 98.8%; Score 761.4; DB 6; Length 771;
 Best Local Similarity 99.2%; Pred. No. 5.3e-116;
 Matches 765; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGCCCCGAGAAAAAAGATCTGGGGGTCAGAGAGCCCCCAGAGAGCAATGGCCCTGG 60
 DB 1 GGGCCCCGAGAAAAAAGATCTGGGGGTCAGAGAGCCCCCAGAGAGCAATGGCCCTGG 60
 QY 61 CAGGTGAGGCTGAGAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 120
 DB 61 CAGGTGAGGCTGAGAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 120
 QY 121 CACCCCAAGTGGTCTGACCCCGCGGCGTGGGGAGCCGAGAGTCAAGGATCTGGCC 180
 DB 121 CACCCCAAGTGGTCTGACCCCGCGGCGTGGGGAGCCGAGAGTCAAGGATCTGGCC 180
 QY 181 GCGCTCAGAGGCTCAAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 240
 DB 181 GCGCTCAGAGGCTCAAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 240
 QY 241 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 CTGGAGCTGGAGAGCGGGTGAAGTCTCCAGCCAGTCCACAGCGGTCAACCCCTGGCCCT 360
 DB 301 CTGGAGCTGGAGAGCGGGTGAAGTCTCCAGCCAGTCCACAGCGGTCAACCCCTGGCCCT 360
 QY 361 GCGTCAAGAGACTTCCCGCGGGGATGCCGTGGTCTGCTGGGGGATGTTGGAGC 420
 DB 361 GCGTCAAGAGACTTCCCGCGGGGATGCCGTGGTCTGCTGGGGGATGTTGGAGC 420
 QY 421 AATGATGAGCGGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCAATATGAA 480
 DB 421 AATGATGAGCGGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCAATATGAA 480
 QY 481 AAGCAATTTGTGACGCAAAATACCACTTTGGCGCTACACGAGAGAGAGAGAGAGAGAG 540
 DB 481 AAGCAATTTGTGACGCAAAATACCACTTTGGCGCTACACGAGAGAGAGAGAGAGAGAG 540
 QY 541 GTCCTGAGAGAGATGCTGTGTGTCGGGGAACACCCGAGAGAGATCATGCCAGGCGACTCC 600
 DB 541 GTCCTGAGAGAGATGCTGTGTGTCGGGGAACACCCGAGAGAGATCATGCCAGGCGACTCC 600
 QY 601 GGAGGGCCCTGCTGTGCAAGGTGAATGAGTGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 GGAGGGCCCTGCTGTGCAAGGTGAATGAGTGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 GCGAGAGGCTGTGCCAGCCCAACCGGCTGCATCTACACCCGCTGCTCACTACTACTTTG 720
 DB 661 GCGAGAGGCTGTGCCAGCCCAACCGGCTGCATCTACACCCGCTGCTCACTACTACTTTG 720

Db 661 GCGAGAGGCTGTGCCAGCCCAACCGGCTGCATCTACACCCGCTGCTCACTACTACTTTG 720
 QY 721 GACTGGATCCACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTTTG 771
 DB 721 GACTGGATCCACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTTTG 771

RESULT 7
 AX347871
 LOCUS AX347871 771 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 38 from Patent WO0198470.
 ACCESSION AX347871
 VERSION AX347871.1 GI:18495678
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Maffei, M., Niles, A.L. and Haak-Frendscho, M.
 TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and
 methods of making same
 JOURNAL Patent: WO 0198470-A 38 27-DEC-2001;
 PROMEGA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7..736
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22429.1"
 /db_xref="GI:18495678"
 /translation="LEKRIVGGQEARPKRPMQVSLRVHGRPMHFGGSLIHQWVW
 TAARVGFVDVLDLALRYQLREQHLXYDQDLPLVSRILVHPQFYTAQGAIALLELE
 EPVYVSSHVHTVLPAPSETRPPGMPGCVTGMGDVNDERLPPPEPLKQVYPIWENH
 ICDARVHGAYTGDDVRIYRDMDCAGNTRDSCQDGGGGLVCKVNGTWMLOAGVYVSW
 GEGCAQPRPPIYTRVRYLLDMIHNYVYKRP"

BASE COUNT 149 a 257 c 241 g 124 t
 ORIGIN
 Query Match 98.5%; Score 759.8; DB 6; Length 771;
 Best Local Similarity 99.1%; Pred. No. 9.7e-116;
 Matches 764; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGCCCCGAGAAAAAAGATCTGGGGGTCAGAGAGCCCCCAGAGAGCAATGGCCCTGG 60
 DB 1 GGGCCCCGAGAAAAAAGATCTGGGGGTCAGAGAGCCCCCAGAGAGCAATGGCCCTGG 60
 QY 61 CAGGTGAGGCTGAGAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 120
 DB 61 CAGGTGAGGCTGAGAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 120
 QY 121 CACCCCAAGTGGTCTGACCCCGCGGCGTGGGGAGCCGAGAGTCAAGGATCTGGCC 180
 DB 121 CACCCCAAGTGGTCTGACCCCGCGGCGTGGGGAGCCGAGAGTCAAGGATCTGGCC 180
 QY 181 GCGCTCAGAGGCTCAAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 240
 DB 181 GCGCTCAGAGGCTCAAGTCCACGAGCCCAATGATGCACTTCTGGGGGGGCTCCCTCATC 240
 QY 241 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 CTGGAGCTGGAGAGCGGGTGAAGTCTCCAGCCAGTCCACAGCGGTCAACCCCTGGCCCT 360
 DB 301 CTGGAGCTGGAGAGCGGGTGAAGTCTCCAGCCAGTCCACAGCGGTCAACCCCTGGCCCT 360
 QY 361 GCGTCAAGAGACTTCCCGCGGGGATGCCGTGGTCTGCTGGGGGATGTTGGAGC 420
 DB 361 GCGTCAAGAGACTTCCCGCGGGGATGCCGTGGTCTGCTGGGGGATGTTGGAGC 420

QY 421 AATGATGAGCCGCTCCACCCGATTTCTCTGTGAAGCAGTGAAGTCCCATTAATGAA 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 AATGATGAGCCGCTCCACCCGATTTCTCTGTGAAGCAGTGAAGTCCCATTAATGAA 480
 QY 481 AACCAATTTGTGACGAAATACCACCTTGGGCGCTPACAGGGAGACAGTCCGATC 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AACCAATTTGTGACGAAATACCACCTTGGGCGCTPACAGGGAGACAGTCCGATC 540
 QY 541 GTCCGTGACAGATGCTGTGTCCGGGAAACACCCGGAGGAGATGATCCAGGGGACTCC 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 GTCCGTGACAGATGCTGTGTCCGGGAAACACCCGGAGGAGATGATCCAGGGGACTCC 600
 QY 601 GGAGGGCCCTGTGTGTGCAAGGTGAAGGCACTGGCTGACAGGGGGCGTGTACAGTGG 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 GGAGGGCCCTGTGTGTGCAAGGTGAAGGCACTGGCTGACAGGGGGCGTGTACAGTGG 660
 QY 661 GGCAGGGCTGTGGCCACCAACCGGCTGGCAATCTACACCCGCTACTACTTG 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 GGCAGGGCTGTGGCCACCAACCGGCTGGCAATCTACACCCGCTACTACTTG 720
 QY 721 GACTGTGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGGCGCGCTCGT 771
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 GACTGTGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGGCGCGCTCGT 771
 RESULT 8
 AX347857 771 bp DNA linear PAR 01-FEB-2002
 LOCUS Sequence 24 from Patent WO0198470.
 DEFINITION AX347857
 ACCESSION AX347857
 VERSION AX347857.1 GI:18495664
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Maffei, M., Niles, A.L. and Haak-Frendscho, M.
 Recombinant proteolytic trypsinases, active site mutants thereof, and
 methods of making same
 Patent: WO 0198470-A 24 27-DEC-2001;
 JOURNAL PROMEGA CORPORATION (US)
 FEATURES
 source Location/Qualifiers
 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7..756
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22422.1"
 /db_xref="GI:18495664"
 /translation="LEKRIYGGDEAPRSKMPWVSLRVHNGPYMMHFGGSLIHPWVLA
 TAHCVGRDVKDLALRVOLBEONLXYODOLLRVSRILVHNPFTADIGADIALLEL
 EPKVVSSHVHTVITLPPASSEFRPGRMPCVWYTKGVDYDDELRPPRPFLKQKYVPLMENN
 ICDKHYHGAYTGDDVRIIVRDMDLCAENTRRDSQGDAGGDLVCKVNGTWLQAGVSM
 GEGCAQPNRPRIYRIVRDMDLCAENTRRDSQGDAGGDLVCKVNGTWLQAGVSM"

Db 121 CACCCCAAGTGGTGTGTGACCCGACCCGACTGCGTGGGACCCGACGTCAGMAGATCTGGCC 180
 QY 181 GCCCTCAGAGGTGCAACTGCGGAGACACACTTACTACTACAGACAGCAGTCTGCGCGGATC 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GCCCTCAGAGGTGCAACTGCGGAGACACACTTACTACTACAGACAGCAGTCTGCGCGGATC 240
 QY 241 AGCAGGATCATCTGACACCCACAGTCTTACACCGCCACAGATGGAAGGAGATGCGCCCTG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 AGCAGGATCATCTGACACCCACAGTCTTACACCGCCACAGATGGAAGGAGATGCGCCCTG 300
 QY 301 CTGGAGCTGGAGGAGCGGAGTGTCTCAGCCAGCCAGCCAGCGTCCACCCCTCC 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 CTGGAGCTGGAGGAGCGGAGTGTCTCAGCCAGCCAGCCAGCGTCCACCCCTCC 360
 QY 361 GCTTCAGAGACTTCCCGCCCGGAGATGCGGTGTGCTGACTGTGGGGGAGATGTGGAC 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 GCTTCAGAGACTTCCCGCCCGGAGATGCGGTGTGCTGACTGTGGGGGAGATGTGGAC 420
 QY 421 AATGATGAGCCCTTCCACCGCCATTTCTGTGAAGCAGTGAAGGTCCCATTAATGAA 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 AATGATGAGCCCTTCCACCGCCATTTCTGTGAAGCAGTGAAGGTCCCATTAATGAA 480
 QY 481 AACCAATTTGTGACGAAATACCACCTTGGGCGCTPACAGGGAGACAGTCCGATC 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AACCAATTTGTGACGAAATACCACCTTGGGCGCTPACAGGGAGACAGTCCGATC 540
 QY 541 GTCCGTGACAGATGCTGTGTCCGGGAAACACCCGGAGGAGATGATCCAGGGGACTCC 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 GTCCGTGACAGATGCTGTGTCCGGGAAACACCCGGAGGAGATGATCCAGGGGACTCC 600
 QY 601 GGAGGGCCCTGTGTGTGCAAGGTGAAGGCACTGGCTGACAGGGGGCGTGTACAGTGG 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 GGAGGGCCCTGTGTGTGCAAGGTGAAGGCACTGGCTGACAGGGGGCGTGTACAGTGG 660
 QY 661 GGCAGGGCTGTGGCCACCAACCGGCTGGCAATCTACACCCGCTACTACTTG 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 GGCAGGGCTGTGGCCACCAACCGGCTGGCAATCTACACCCGCTACTACTTG 720
 QY 721 GACTGTGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGGCGCGCTCGT 771
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 GACTGTGATCCACCACTATGTCCCAAAAAGCCGTGAAGCGGCGCGCTCGT 771
 RESULT 9
 AX347859 771 bp DNA linear PAR 01-FEB-2002
 LOCUS Sequence 26 from Patent WO0198470.
 DEFINITION AX347859
 ACCESSION AX347859
 VERSION AX347859.1 GI:18495666
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Maffei, M., Niles, A.L. and Haak-Frendscho, M.
 Recombinant proteolytic trypsinases, active site mutants thereof, and
 methods of making same
 Patent: WO 0198470-A 26 27-DEC-2001;
 JOURNAL PROMEGA CORPORATION (US)
 FEATURES
 source Location/Qualifiers
 1..771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7..756
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22423.1"
 /db_xref="GI:18495666"
 /translation="LEKRIYGGDEAPRSKMPWVSLRVHNGPYMMHFGGSLIHPWVLA
 TAHCVGRDVKDLALRVOLBEONLXYODOLLRVSRILVHNPFTADIGADIALLEL
 EPKVVSSHVHTVITLPPASSEFRPGRMPCVWYTKGVDYDDELRPPRPFLKQKYVPLMENN
 ICDKHYHGAYTGDDVRIIVRDMDLCAENTRRDSQGDAGGDLVCKVNGTWLQAGVSM"

BASE COUNT 152 a 255 c 241 g 123 t

ORIGIN

Query Match 97.9%; Score 755; DB 6; Length 771; Best Local Similarity 98.7%; Pred. No. 6e-115; Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

1 GGGCCCCCTCGAGAAAAGATGCTGGGGGTCAGAGAGCCCGGAGGAAAGTGGCCCTGG 60
1 GGGCCCCCTCGAGAAAAGATGCTGGGGGTCAGAGAGCCCGGAGGAAAGTGGCCCTGG 60
61 CAGGTGAGCCCTGAGAGTCCACGCCCATPACTGATGCACTTCTGGCGGGGCTCCCTCATC 120
61 CAGGTGAGCCCTGAGAGTCCACGCCCATPACTGATGCACTTCTGGCGGGGCTCCCTCATC 120
121 CACCCCAAGTGGTGTGACCCGCGCGGCTGCGTGGGACCGGACAGTCAAGATTTGGCC 180
121 CACCCCAAGTGGTGTGACCCGCGCGGCTGCGTGGGACCGGACAGTCAAGATTTGGCC 180
181 GCCCTCAGGGTGCACACTGCGGGGAGCAGCCTCTACTACCAAGCAGCGTGGCCGGTGC 240
181 GCCCTCAGGGTGCACACTGCGGGGAGCAGCCTCTACTACCAAGCAGCGTGGCCGGTGC 240
241 AGCAGGATCATGCTGACCCACAGTTCCTACACCGCCAGANTGAGCGGACATCGCCCTG 300
241 AGCAGGATCATGCTGACCCACAGTTCCTACACCGCCAGANTGAGCGGACATCGCCCTG 300
301 CTGGAGCTGGAGGACCGGTGAGGTCTCCAGCCACGTCACAGCGTCACTGCCCTT 360
301 CTGGAGCTGGAGGACCGGTGAGGTCTCCAGCCACGTCACAGCGTCACTGCCCTT 360
361 GCCTCAGAGACCTTCCCGCCGGGAGTCCGCTGCTGGTCACTGGCTGGCGATGGAGC 420
361 GCCTCAGAGACCTTCCCGCCGGGAGTCCGCTGCTGGTCACTGGCTGGCGATGGAGC 420
421 AATGATGAGCGCCCTCCACCGCCATTTCTTGAAGCAGGTGAAGTCCCTTAATGGA 480
421 AATGATGAGCGCCCTCCACCGCCATTTCTTGAAGCAGGTGAAGTCCCTTAATGGA 480
481 AACCCATTGTTGAGGCAAAATPACCACTTGGCGCTACACCGGAGACAGCCTCCGCATC 540
481 AACCCATTGTTGAGGCAAAATPACCACTTGGCGCTACACCGGAGACAGCCTCCGCATC 540
541 GTCCCTGAGACACTGCTGTGTGCGGGGAAACACCGGAGGAACTCAMPGCCAGGGCAATCC 600
541 GTCCCTGAGACACTGCTGTGTGCGGGGAAACACCGGAGGAACTCAMPGCCAGGGCAATCC 600
601 GGAGGGCCCTGCTGTGCAAGGTGAATGACACCTGCTGCAGAGCGGGGCTGCTGACTGG 660
601 GGAGGGCCCTGCTGTGCAAGGTGAATGACACCTGCTGCAGAGCGGGGCTGCTGACTGG 660
661 GGCGAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACCCCGTGTCACTACTGTTG 720
661 GGCGAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACCCCGTGTGTCACTACTGTTG 720
721 GACTGATTCACCACTATGTCCCAAAAAAGCGGTGAAGGGCGCCGCTGGT 771
721 GACTGATTCACCACTATGTCCCAAAAAAGCGGTGAAGGGCGCCGCTGGT 771

RESULT 10
AX347873 AX347873 771 bp DNA linear PAT 01-FEB-2002
LOCUS AX347873
DEFINITION Sequence 40 from Patent W00198470.
ACCESSION AX347873
VERSION AX347873.1 GI:18495680
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Maffei, M., Niles, A. L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and
METHODS methods of making same
JOURNAL Patent: WO 0198470-A 40 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..771
/organism="Homo sapiens"
<db_xref="taxon:9606"
<1..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22430.1"
/db_xref="GI:18495681"
/translation="GPLEKRIYGGGQFAPRPSKMPWQVSLRVHGRPYMHRFGGSLIHPQW
VLTAAKVGPRVYKLAALRVDLRKQHLIYDQILVPSRIIYHPPTAOLGADTALIE
LEBPYVSSHVHTVTLPPASFTFPPGMEVGGVDVNDNDRLLRPPPLRQVYPIE
NHICDANKHLAAYTGDDVRIYRDMILAGNTRRSDCGDAGGPLVCKRVNGTMIQAGVY
SMGEGCAQPNRPDIYTRVYIYLDVIMHHVYVPRKP"

BASE COUNT 150 a 256 c 240 g 125 t
ORIGIN
Query Match 97.7%; Score 753.4; DB 6; Length 771;
Best Local Similarity 98.6%; Pred. No. 1.1e-114;
Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1 GGGCCCCCTCGAGAAAAGATGCTGGGGGTCAGAGAGCCCGGAGGAAAGTGGCCCTGG 60
1 GGGCCCCCTCGAGAAAAGATGCTGGGGGTCAGAGAGCCCGGAGGAAAGTGGCCCTGG 60
61 CAGGTGAGCCCTGAGAGTCCACGCCCATPACTGATGCACTTCTGGCGGGGCTCCCTCATC 120
61 CAGGTGAGCCCTGAGAGTCCACGCCCATPACTGATGCACTTCTGGCGGGGCTCCCTCATC 120
121 CACCCCAAGTGGTGTGACCCGCGCGGCTGCGTGGGACCGGACAGTCAAGATTTGGCC 180
121 CACCCCAAGTGGTGTGACCCGCGCGGCTGCGTGGGACCGGACAGTCAAGATTTGGCC 180
181 GCCCTCAGGGTGCACACTGCGGGGAGCAGCCTCTACTACCAAGCAGCGTGGCCGGTGC 240
181 GCCCTCAGGGTGCACACTGCGGGGAGCAGCCTCTACTACCAAGCAGCGTGGCCGGTGC 240
241 AGCAGGATCATGCTGACCCACAGTTCCTACACCGCCAGANTGAGCGGACATCGCCCTG 300
241 AGCAGGATCATGCTGACCCACAGTTCCTACACCGCCAGANTGAGCGGACATCGCCCTG 300
301 CTGGAGCTGGAGGACCGGTGAGGTCTCCAGCCACGTCACAGCGTCACTGCCCTT 360
301 CTGGAGCTGGAGGACCGGTGAGGTCTCCAGCCACGTCACAGCGTCACTGCCCTT 360
361 GCCTCAGAGACCTTCCCGCCGGGAGTCCGCTGCTGGTCACTGGCTGGCGATGGAGC 420
361 GCCTCAGAGACCTTCCCGCCGGGAGTCCGCTGCTGGTCACTGGCTGGCGATGGAGC 420
421 AATGATGAGCGCCCTCCACCGCCATTTCTTGAAGCAGGTGAAGTCCCTTAATGGA 480
421 AATGATGAGCGCCCTCCACCGCCATTTCTTGAAGCAGGTGAAGTCCCTTAATGGA 480
481 AACCCATTGTTGAGGCAAAATPACCACTTGGCGCTACACCGGAGACAGCCTCCGCATC 540
481 AACCCATTGTTGAGGCAAAATPACCACTTGGCGCTACACCGGAGACAGCCTCCGCATC 540
541 GTCCCTGAGACACTGCTGTGTGCGGGGAAACACCGGAGGAACTCAMPGCCAGGGCAATCC 600
541 GTCCCTGAGACACTGCTGTGTGCGGGGAAACACCGGAGGAACTCAMPGCCAGGGCAATCC 600
601 GGAGGGCCCTGCTGTGCAAGGTGAATGACACCTGCTGCAGAGCGGGGCTGCTGACTGG 660
601 GGAGGGCCCTGCTGTGCAAGGTGAATGACACCTGCTGCAGAGCGGGGCTGCTGACTGG 660
661 GGCGAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACCCCGTGTGTCACTACTGTTG 720
661 GGCGAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACCCCGTGTGTCACTACTGTTG 720

RESULT 10
AX347873 AX347873 771 bp DNA linear PAT 01-FEB-2002
LOCUS AX347873
DEFINITION Sequence 40 from Patent W00198470.
ACCESSION AX347873
VERSION AX347873.1 GI:18495680
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

QY 721 GACTGGATCCACCCTATGTGCCCAAAAAGCCGTGAAGCGCCCGCTCGT 771
 |||
 Db 721 GACTGGATCCACCCTATGTGCCCAAAAAGCCGTGAAGCGCCCGCTCGT 771

RESULT 11
 AX347875 771 bp DNA linear PAT 01-FBB-2002
 LOCUS Sequence 42 from Patent WO0198470.
 AX347875
 ACCESION AX347875
 VERSION AX347875.1 GI:18495682
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Maifit, M., Niles, A.L. and Haak-Frendscho, M.
 Recombinant proteolytic trypsinases, active site mutants thereof, and
 methods of making same
 Patent: WO 0198470-A 42 27-DEC-2001:
 JOURNAL PROMEGA CORPORATION (US)
 LOCATION/Qualifiers
 source 1. 771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <7. 756
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22431.1"
 /db_xref="GI:18495683"
 /translation="LEKRIYGGQEARSKRPMQVSLVHNGRYMMHFGGSLIHPQWV
 /TAHCVGRDYKDLALRYOLREOHLYODDILPVSRIIVHROYTADIGADILLELE
 EPNVSSHVHTVLPASSETRPMPGMRVMTGMDVDNDELRLPRLPKQKVPDMEVH
 ICDAKHLGATGDDVRYTVDMLCSAGNTRDSDQSDAGSPLVCKVNGTLDQAGVYS
 GEGCAQDRPRGIYTRVYLYLDWIMHNYPKRP"

BASE COUNT 152 a 256 c 240 g 123 t
 ORIGIN

Query Match 97.7%: Score 753.4; DB 6; Length 771;
 Best Local Similarity 96.6%; Pred. No. 1.1e-114;
 Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAGAAAAGATCGTGGGGGTGAGAGGCCCCAGAGCAAGTGGCCCTGG 60
 |||
 Db 1 GGGCCCTCGAGAAAAGATCGTGGGGGTGAGAGGCCCCAGAGCAAGTGGCCCTGG 60

QY 61 CAGGTGAGCCCTGAGAGTCCACGGCCCAATCTGATGATGCACCTTCCTGGGGCTCCCTCATC 120
 |||
 Db 61 CAGGTGAGCCCTGAGAGTCCACGGCCCAATCTGATGATGCACCTTCCTGGGGCTCCCTCATC 120

QY 121 CACCCCAAGTGGGTCTGATACCGCGCGGGCGTGGGGAGACCGGATCAAGGATGTGGCC 180
 |||
 Db 121 CACCCCAAGTGGGTCTGATACCGCGCGGGCGTGGGGAGACCGGATCAAGGATGTGGCC 180

QY 181 GCCCTCAGAGGTCACACTGCGGAGGAGCACCCTCTACTACCAAGGACCACTGGTCCGGGCT 240
 |||
 Db 181 GCCCTCAGAGGTCACACTGCGGAGGAGCACCCTCTACTACCAAGGACCACTGGTCCGGGCT 240

QY 241 AGCAGGATCATGTGTCACCAAGTTCATACACCGCCCAAGATCGAGAGCGGATTCGCCCTG 300
 |||
 Db 241 AGCAGGATCATGTGTCACCAAGTTCATACACCGCCCAAGATCGAGAGCGGATTCGCCCTG 300

QY 301 CTGAGCTGGAGAGAGCGGCTGAAGTCTTCACGCAACGTCACACAGGATTCAGCCCTGGCCCT 360
 |||
 Db 301 CTGAGCTGGAGAGAGCGGCTGAAGTCTTCACGCAACGTCACACAGGATTCAGCCCTGGCCCT 360

QY 361 GCCTCAGAGAACCTTCCCGCCGGGAGTCCCTGGTCTGACTGCTGGGGGCGATGTGGAC 420
 |||
 Db 361 GCCTCAGAGAACCTTCCCGCCGGGAGTCCCTGGTCTGACTGCTGGGGGCGATGTGGAC 420

QY 421 AATGATGAGCGCCCTCCACCGCCATTTCCTCTGAAAGCAGGATGAGGATCCCATTAATGAAA 480

Db 421 AATGATGAGCGCCCTCCACCGCCATTTCCTCTGAAAGCAGGATGAGGATCCCATTAATGAAA 480
 |||
 QY 481 AACCACTTTGTGACCGCAAAATACACAGCTTGGCCCTACAGGGAGAGAGAGCTCCGATC 540
 |||
 Db 481 AACCACTTTGTGACCGCAAAATACACAGCTTGGCCCTACAGGGAGAGAGAGCTCCGATC 540

QY 541 GTCCTGACAGCAATGCTGTGTGTCGGGGGACACCGCGGAGGAGTCAAGGAGGAGGAGTCC 600
 |||
 Db 541 GTCCTGACAGCAATGCTGTGTGTCGGGGGACACCGCGGAGGAGTCAAGGAGGAGGAGTCC 600

QY 601 GGAGGGCCCTGGTGTGCAAGAGTGAATGGACCTGGCTGAGCGGGCGGTGTCACTGAG 660
 |||
 Db 601 GGAGGGCCCTGGTGTGCAAGAGTGAATGGACCTGGCTGAGCGGGCGGTGTCACTGAG 660

QY 661 GCGGAGCACTGCTGTGTGTCAGAAAGTGGAAATGGACCTGGCTGAGCGGGCGGTGTCACTGAG 660
 |||
 Db 661 GCGGAGCACTGCTGTGTGTCAGAAAGTGGAAATGGACCTGGCTGAGCGGGCGGTGTCACTGAG 660

QY 721 GACTGGATCCACCCTATGTGCCCAAAAAGCCGTGAAGCGCCCGCTCGT 771
 |||
 Db 721 GACTGGATCCACCCTATGTGCCCAAAAAGCCGTGAAGCGCCCGCTCGT 771

RESULT 12
 AX347861 735 bp DNA linear PAT 01-FBB-2002
 LOCUS Sequence 28 from Patent WO0198470.
 AX347861
 ACCESION AX347861
 VERSION AX347861.1 GI:18495668
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Maifit, M., Niles, A.L. and Haak-Frendscho, M.
 Recombinant proteolytic trypsinases, active site mutants thereof, and
 methods of making same
 Patent: WO 0198470-A 28 27-DEC-2001:
 JOURNAL PROMEGA CORPORATION (US)
 LOCATION/Qualifiers
 source 1. 735
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <1. >7/35
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22424.1"
 /translation="IVGGQEARPRSKRPMQVSLVHNGRYMMHFGGSLIHPQWVLTAA
 /CVGPDVLDLALRYOLREOHLYODDILPVSRIIVHROYTADIGADILLELEEVK
 VSSHVHTVLPASSETRPMPGMRVMTGMDVDNDELRLPRLPKQKVPDMEVHICDA
 KYHLAGATGDDVRYTVDMLCSAGNTRDSDQSDAGSPLVCKVNGTLDQAGVYSWGBGC
 AQRPRGIYTRVYLYLDWIMHNYPKRP"

BASE COUNT 139 a 245 c 231 g 120 t
 ORIGIN

Query Match 95.3%: Score 735; DB 6; Length 735;
 Best Local Similarity 100.0%; Pred. No. 1.2e-111;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ATCTGTCGGGGGTGACGAGGAGCCCGCCAGAGCAAGTGGCCCTGAGAGTCAAGAGTTC 78
 |||
 Db 19 ATCTGTCGGGGGTGACGAGGAGCCCGCCAGAGCAAGTGGCCCTGAGAGTCAAGAGTTC 78

QY 79 CACGGCCATCTGATGATCACTTCGCGGGGCTCCCTCATCAACCCAGTGGGTGGCTG 138
 |||
 Db 79 CACGGCCATCTGATGATCACTTCGCGGGGCTCCCTCATCAACCCAGTGGGTGGCTG 120

QY 139 ACCGGCCGGCGCTGGCTGGAGACCGGAGCTCAAGAGTCTGGCCCGCTCAAGGATGCAACTG 198
 |||
 Db 121 ACCGGCCGGCGCTGGCTGGAGACCGGAGCTCAAGAGTCTGGCCCGCTCAAGGATGCAACTG 180

QY 199 CGGAGCAGCACCTCTACTACCAGGACCAGCTGTCCGGTCCAGCAGGATCATCTGGAC 258
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGTCCGGTCCAGCAGGATCATCTGGAC 240
 QY 259 CCACAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 318
 Db 241 CCACAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 300
 QY 319 GTGAAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 378
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 GTGAAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 360
 QY 379 CCGGGGATCCGCTGTGGGATCAGTCCGCTGGGGGATGAGCAATGATGAGCCCTCCA 438
 Db 361 CCGGGGATCCGCTGTGGGATCAGTCCGCTGGGGGATGAGCAATGATGAGCCCTCCA 420
 QY 439 CCGCCATTCTCTGAGAGCAGGTGAAGTCCCAATATGAAACACCATTTTGTGACGCA 498
 Db 421 CCGCCATTCTCTGAGAGCAGGTGAAGTCCCAATATGAAACACCATTTTGTGACGCA 480
 QY 499 AAATACACCTTTGGGCTTACACGGGAGACGACGTCGCCATGCTCCGTGACATGCTG 558
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AAATACACCTTTGGGCTTACACGGGAGACGACGTCGCCATGCTCCGTGACATGCTG 540
 QY 559 TGTGCCGGGAACACCCGGAGGACTCATGCCAGGCGACTCCGGAGGGCCCTGTGTGC 618
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 TGTGCCGGGAACACCCGGAGGACTCATGCCAGGCGACTCCGGAGGGCCCTGTGTGC 600
 QY 619 AAGGTGAATGACACCTGCTGAGGCGGGCGTGTGACCTGGGGCGAGGGCTGTGCCAG 678
 Db 601 AAGGTGAATGACACCTGCTGAGGCGGGCGTGTGACCTGGGGCGAGGGCTGTGCCAG 660
 QY 679 CCGAACCAGGCGGCTGATACACCCGCTGACCTACTTGGATGATCCACCATAT 738
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 CCGAACCAGGCGGCTGATACACCCGCTGACCTACTTGGATGATCCACCATAT 720
 QY 739 GTCCCAAAAAAGCCG 735
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 GTCCCAAAAAAGCCG 735

RESULT 13
 AX347877 735 bp DNA Linear PAT 01-FEB-2002
 LOCUS AX347877
 DEFINITION Sequence 44 from Patent WO0198470.
 ACCESSION AX347877.1 GI:18495684
 VERSION AX347877.1 GI:18495684
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 Mafli, M., Niles, A.L. and Haak-Frendscho, M.
 Recombinant proteolytic tryptases, active site mutants thereof, and
 methods of making same
 Patent: WO 0198470-A 44 27-DEC-2001;
 JOURNAL PROMEGA CORPORATION (US)
 TITLE Location/Qualifiers
 FEATURES
 source
 1..735
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 <1..>735
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22432.1"
 /db_xref="gi:18495685"
 /translation="IYGGQEA PRSKPMPQVSLRVHGPVYWHMFGGSLIHPQWVLTAA
 CVGSDVKDIALRIVLRKHLYKODLLPVSRIIVYHFOYTRADLALILEPVA
 VSSVHVVYLPASETRPGRPCWYIGVDVNDERLPPPLKOVKPIENHICDA
 KYHIGAVYGDVRIIVRDMICAGNTRRDSGCGDGGPLVKNVNGTMDLAGVYVSGEGC
 AQPNRPGIYRIVRYIYLDVIMHIVPKKP"

BASE COUNT 139 a 246 c 230 g 120 t
 ORIGIN
 Query Match 95.1%; Score 733.4; DB 6; Length 735;
 Best Local Similarity 99.9%; Pred. No. 2.2e-111;
 Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 19 ATGTCGGGGGTCCAGGAGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGTC 78
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGTCGGGGGTCCAGGAGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGTC 60
 QY 79 CACGGCCCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 138
 Db 61 CACGGCCCATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 QY 139 ACCGGCCGGGCGCTGGTGGGACCCGAGCTCAAGATGTCGGCCCTCAAGGCTGACTG 198
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ACCGGCCGGGCGCTGGTGGGACCCGAGCTCAAGATGTCGGCCCTCAAGGCTGACTG 180
 QY 199 CCGGAGCAGCACCTCTACTACCAGGACCAGCTGTCCGGTCCAGCAGGATCATCTGGAC 258
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CCGGAGCAGCACCTCTACTACCAGGACCAGCTGTCCGGTCCAGCAGGATCATCTGGAC 240
 QY 259 CCACAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 318
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CCACAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 300
 QY 319 GTGAAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 378
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 GTGAAGTTCCTACACCCGCCAGATGCGGAGCGGACATCCCTCTGTGGAGGAGCCG 360
 QY 379 CCGGGGATCCGCTGTGGGATCAGTCCGCTGGGGGATGAGCAATGATGAGCCCTCCA 438
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 CCGGGGATCCGCTGTGGGATCAGTCCGCTGGGGGATGAGCAATGATGAGCCCTCCA 420
 QY 439 CCGCCATTCTCTGAGAGCAGGTGAAGTCCCAATATGAAACACCATTTTGTGACGCA 498
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 CCGCCATTCTCTGAGAGCAGGTGAAGTCCCAATATGAAACACCATTTTGTGACGCA 480
 QY 499 AAATACACCTTTGGGCTTACACGGGAGACGACGTCGCCATGCTCCGTGACATGCTG 558
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AAATACACCTTTGGGCTTACACGGGAGACGACGTCGCCATGCTCCGTGACATGCTG 540
 QY 559 TGTGCCGGGAACACCCGGAGGACTCATGCCAGGCGACTCCGGAGGGCCCTGTGTGC 618
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 TGTGCCGGGAACACCCGGAGGACTCATGCCAGGCGACTCCGGAGGGCCCTGTGTGC 600
 QY 619 AAGGTGAATGACACCTGCTGAGGCGGGCGTGTGACCTGGGGCGAGGGCTGTGCCAG 678
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 AAGGTGAATGACACCTGCTGAGGCGGGCGTGTGACCTGGGGCGAGGGCTGTGCCAG 660
 QY 679 CCGAACCAGGCGGCTGATACACCCGCTGACCTACTTGGATGATCCACCATAT 738
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 CCGAACCAGGCGGCTGATACACCCGCTGACCTACTTGGATGATCCACCATAT 720
 QY 739 GTCCCAAAAAAGCCG 735
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 GTCCCAAAAAAGCCG 735

RESULT 14
 AR080461 1128 bp DNA Linear PAT 31-AUG-2000
 LOCUS AR080461
 DEFINITION Sequence 15 from patent US 5968782.
 ACCESSION AR080461
 VERSION AR080461.1 GI:10007196
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 Unclassified.
 AUTHORS Stevens, R.L.
 TITLE Mast cell protease that cleaves fibrinogen

JOURNAL Patent: US 596782-A 15 19-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..1128
 BASE COUNT 190 a 409 c 329 g 200 t
 ORIGIN

Query Match 94.8%; Score 731; DB 6; Length 1128;
 Best Local Similarity 98.7%; Pred. No. 5.1e-111;
 Matches 737; Conservatvie 0; Mismatches 10; Indels 0; Gaps 0;

Oy 17 GAATGTCGGGGGTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGAG 76
 Db 87 GCATCGTGGGGGTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGAG 146
 Oy 77 TCCAGCGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 136
 Db 147 TCCAGCGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATG 206
 Oy 137 TGACCG 196
 Db 207 TGACCG 266
 Oy 197 TGGCGGAGACACACCTCTACTACTACTACTACTACTACTACTACTACTACT 256
 Db 267 TGGCGGAGACACACCTCTACTACTACTACTACTACTACTACTACTACTACT 326
 Oy 257 ACCCGAGTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 316
 Db 327 ACCCGAGTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 386
 Oy 317 CGGTGAAGGTCTCCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 376
 Db 387 CGGTGAAGGTCTCCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 446
 Oy 377 CCCCCGGGATGCGCTGTGGGTCTACTGCTGTGGGCGGATGTGGACAATGAG 436
 Db 447 CCCCCGGGATGCGCTGTGGGTCTACTGCTGTGGGCGGATGTGGACAATGAG 506
 Oy 437 CACCGCCATTTCTCTGTAAGGACGGTGAAGGATGCGGATGCGGATGCGG 496
 Db 507 CACCGCCATTTCTCTGTAAGGACGGTGAAGGATGCGGATGCGGATGCGG 566
 Oy 497 CAATAATACACCTTGGCCCTTACACAGGAGAGCAGCAGCAGCAGCAGCAGC 556
 Db 567 CAATAATACACCTTGGCCCTTACACAGGAGAGCAGCAGCAGCAGCAGCAGC 626
 Oy 557 TGTGTGGCGGAAACACCGGAGGAGCTATGCTGAGGCGGAGTCCGGGCTGT 616
 Db 627 TGTGTGGCGGAAACACCGGAGGAGCTATGCTGAGGCGGAGTCCGGGCTGT 686
 Oy 617 GCAAGGTGAATGCGACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 676
 Db 687 GCAAGGTGAATGCGACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 746
 Oy 677 AGCCCAACCGGCTGGATCTACACAGCAGCAGCAGCAGCAGCAGCAGCAG 736
 Db 747 AGCCCAACCGGCTGGATCTACACAGCAGCAGCAGCAGCAGCAGCAGCAG 806
 Oy 737 ATGTCCCAAAAAAGCGGTGAAGCGGCG 763
 Db 807 ATGTCCCAAAAAAGCGGTGAAGCGGCG 833

RESULT 15
 HUMTRY2A 1128 bp mRNA linear PRI 03-AUG-1993
 LOCUS Human tryptase-II mRNA, 3' end.
 DEFINITION Human tryptase-II.
 ACCESSION M33492.1 GI:339982
 VERSION M33492.1 GI:339982
 KEYWORDS serine protease; tryptase-II.
 SOURCE Human adult skin, cDNA to mRNA.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinda; Homo. 1 (bases 1 to 1128)
 AUTHORS VanderSlie, P., Ballinger, S.M., Tam, E.K., Goldstein, S.M., Craik, C.S. and Caughey, G.H.
 TITLE Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine protease family
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (10), 3811-3815 (1990)
 MEDLINE 90251647
 PUBMED 2187193
 COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by P. VanderSlie, 02-APR-1990.
 location/Qualifiers
 1..1128

FEATURES source
 CDS
 <1..826
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="tryptase-II"
 /codon_start=2
 /protein_id="AAA36779.1"
 /db_xref="GI:339983"
 /translation="MRLLLALPVLASRAVAAPAPQALQRVGIVGSGEAPRKKWPMQVSLRKHGPIYMHHPGGSLIHPOWVLAHCVGPDVYKDLALRQLRPHLHYDQLPVSIRVHPQPTAQIGADIALLELEEVKVSSSHVHTLTPASETPPPKPCWYTGSDVNDERLPPFPFKQYKPIEMENHEDAKYHNGAYGYDRTVIRDDMLCAGMTRBSCQSGSGPFLVCKVMGTWLDQGVVSWGSCAQPNRPGIYRVTYLDLHIVYVKKP"
 polyA_signal 1121..1126
 BASE COUNT 190 a 409 c 329 g 200 t
 ORIGIN

Query Match 94.8%; Score 731; DB 9; Length 1128;
 Best Local Similarity 98.7%; Pred. No. 5.1e-111;
 Matches 737; Conservatvie 0; Mismatches 10; Indels 0; Gaps 0;

Oy 17 GAATGTCGGGGGTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGAG 76
 Db 87 GCATCGTGGGGGTCAGAGAGCCGCCAGAGCAAGTGGCCCTGGCAGGTGAGAG 146
 Oy 77 TCCAGCGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 136
 Db 147 TCCAGCGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATG 206
 Oy 137 TGACCG 196
 Db 207 TGACCG 266
 Oy 197 TGGCGGAGACACACCTCTACTACTACTACTACTACTACTACTACTACTACT 256
 Db 267 TGGCGGAGACACACCTCTACTACTACTACTACTACTACTACTACTACTACT 326
 Oy 257 ACCCGAGTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 316
 Db 327 ACCCGAGTTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 386
 Oy 317 CGGTGAAGGTCTCCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 376
 Db 387 CGGTGAAGGTCTCCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 446
 Oy 377 CCCCCGGGATGCGCTGTGGGTCTACTGCTGTGGGCGGATGTGGACAATGAG 436
 Db 447 CCCCCGGGATGCGCTGTGGGTCTACTGCTGTGGGCGGATGTGGACAATGAG 506
 Oy 437 CACCGCCATTTCTCTGTAAGGACGGTGAAGGATGCGGATGCGGATGCGG 496
 Db 507 CACCGCCATTTCTCTGTAAGGACGGTGAAGGATGCGGATGCGGATGCGG 566
 Oy 497 CAATAATACACCTTGGCCCTTACACAGGAGAGCAGCAGCAGCAGCAGCAGC 556
 Db 567 CAATAATACACCTTGGCCCTTACACAGGAGAGCAGCAGCAGCAGCAGCAGC 626
 Oy 557 TGTGTGGCGGAAACACCGGAGGAGCTATGCTGAGGCGGAGTCCGGGCTGT 616

Db 627 TGTGTCCGGGAACACCCGGAGGACTCATGCCAGGGCCACTCCGGAGGGCCCTGTGTGT 686
OY 617 GCAAGGTGAATGGCACACTGGCTGCAGCGCGGGCTGTGTCAGTGGGGCCGAGGGCTGTGCC 676
Db 687 GCAAGGTGAATGGCACACTGGCTGCAGCGCGGGCTGTGTCAGTGGGGCCGAGGGCTGTGCC 746
OY 677 AGCCCAACCGGCTGGCACTTACACCCGTTGTCACCTACTTGGACTGGATCCACCACT 736
Db 747 AGCCCAACCGGCTGGCACTTACACCCGTTGTCACCTACTTGGACTGGATCCACCACT 806
OY 737 ATGTCCCAAAAAGCCGTGAAGCGGCC 763
Db 807 ATGTCCCAAAAAGCCGTGAAGCGGCC 833

Search completed: January 31, 2003, 06:12:33
Job time : 2817 secs

